

7.0 SEQUENCE LISTING

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANT: Baum, James A.
 Gilmer, Amy Jelen
 Mettus, Anne-Marie Light

10 (ii) TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
LEPIDOPTERAN-ACTIVE- δ -ENDOTOXINS

(iii) NUMBER OF SEQUENCES: 76

15 (iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Almold, White & Durkee
- (B) STREET: P.O. Box 4433
- (C) CITY: Houston
- (D) STATE: Texas
- (E) COUNTRY: USA
- (F) ZIP: 77210

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

30 (A) APPLICATION NUMBER: US Unknown
(B) FILING DATE:
(C) CLASSIFICATION: Unknown

(vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: US 08/757,536
(B) FILING DATE: 27-NOV-1996

(viii) ATTORNEY/AGENT INFORMATION:

(ix) TELECOMMUNICATION INFORMATION:

45 (A) TELEPHONE: 512/418-3000
(B) TELEFAX: 512/474-7577

(2) INFORMATION FOR SEQ ID NO:1:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3567 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..3567

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

10	ATG GAG GAA AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser 1 5 10 15	48
15	AAT CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA ACT GGT AAT Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn 20 25 30	96
20	TCA TCA ATT GAT ATT TCT CTG TCA CTT GTT CAG TTT CTG GTA TCT AAC Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn 25 35 40 45	144
25	TTT GTA CCA GGG GGA GGA TTT TTA GTT GGA TTA ATA GAT TTT GTA TGG Phe Val Pro Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp 30 50 55 60	192
30	GGA ATA GTT GGC CCT TCT CAA TGG GAT GCA TTT CTA GTA CAA ATT GAA Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu 35 65 70 75 80	240
35	CAA TTA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT GCT ATT Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile 40 85 90 95	288
40	GCT AAT TTA GAA GGA TTA GGA AAC AAT TTC AAT ATA TAT GTG GAA GCA Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala 45 100 105 110	336
45	TTT AAA GAA TGG GAA GAA GAT CCT AAT AAT CCA GCA ACC AGG ACC AGA Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg 50 115 120 125	384
50	GTA ATT GAT CGC TTT CGT ATA CTT GAT GGG CTA CTT GAA AGG GAC ATT Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile 55 130 135 140	432
55	CCT TCG TTT GCA ATT TCT GGA TTT GAA GTA CCC CTT TTA TCC GTT TAT Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr 60 145 150 155 160	480
60	GCT CAA GCG GCC AAT CTG CAT CTA GCT ATA TTA AGA GAT TCT GTA ATT Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile 65 165 170 175	528

	TTT GGA GAA AGA TGG GGA TTG ACA ACG ATA AAT GTC AAT GAA AAC TAT Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr	576
	180 185 190	
5	AAT AGA CTA ATT AGG CAT ATT GAT GAA TAT GCT GAT CAC TGT GCA AAT Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn	624
	195 200 205	
10	ACG TAT AAT CGG GGA TTA AAT AAT TTA CCG AAA TCT ACG TAT CAA GAT Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp	672
	210 215 220	
15	TGG ATA ACA TAT AAT CGA TTA CGG AGA GAC TTA ACA TTG ACT GTA TTA Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu	720
	225 230 235 240	
20	GAT ATC GCC GCT TTC TTT CCA AAC TAT GAC AAT AGG AGA TAT CCA ATT Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile	768
	245 250 255	
25	CAG CCA GTT GGT CAA CTA ACA AGG GAA GTT TAT ACG GAC CCA TTA ATT Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile	816
	260 265 270	
30	AAT TTT AAT CCA CAG TTA CAG TCT GTA GCT CAA TTA CCT ACT TTT AAC Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn	864
	275 280 285	
35	GTT ATG GAG AGC AGC GCA ATT AGA AAT CCT CAT TTA TTT GAT ATA TTG Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu	912
	290 295 300	
40	AAT AAT CTT ACA ATC TTT ACG GAT TGG TTT AGT GTT GGA CGC AAT TTT Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe	960
	305 310 315 320	
45	TAT TGG GGA GGA CAT CGA GTA ATA TCT AGC CTT ATA GGA GGT GGT AAC Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Asn	1008
	325 330 335	
50	ATA ACA TCT CCT ATA TAT GGA AGA GAG GCG AAC CAG GAG CCT CCA AGA Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg	1056
	340 345 350	
55	TCC TTT ACT TTT AAT GGA CCG GTA TTT AGG ACT TTA TCA AAT CCT ACT Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr	1104
	355 360 365	
60	TTA CGA TTA TTA CAG CAA CCT TGG CCA GCG CCA CCA TTT AAT TTA CGT Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg	1152
	370 375 380	

	GGT GTT GAA GGA GTA GAA TTT TCT ACA CCT ACA AAT AGC TTT ACG TAT Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr 385 390 395 400	1200
5	CGA GGA AGA GGT ACG GTT GAT TCT TTA ACT GAA TTA CCG CCT GAG GAT Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp 405 410 415	1248
10	AAT AGT GTG CCA CCT CGC GAA GGA TAT AGT CAT CGT TTA TGT CAT GCA Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala 420 425 430	1296
15	ACT TTT GTT CAA AGA TCT GGA ACA CCT TTT TTA ACA ACT GGT GTA GTA Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val 435 440 445	1344
20	TTT TCT TGG ACG CAT CGT AGT GCA ACT CTT ACA AAT ACA ATT GAT CCA Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro 450 455 460	1392
25	GAG AGA ATT AAT CAA ATA CCT TTA GTG AAA GGA TTT AGA GTT TGG GGG Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly 465 470 475 480	1440
30	GGC ACC TCT GTC ATT ACA GGA CCA GGA TTT ACA GGA GGG GAT ATC CTT Gly Thr Ser Val Ile Thr Gly Pro Phe Thr Gly Gly Asp Ile Leu 485 490 495	1488
35	CGA AGA AAT ACC TTT GGT GAT TTT GTA TCT CTA CAA GTC AAT ATT AAT Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn 500 505 510	1536
40	TCA CCA ATT ACC CAA AGA TAC CGT TTA AGA TTT CGT TAC GCT TCC AGT Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser 515 520 525	1584
45	AGG GAT GCA CGA GTT ATA GTA TTA ACA GGA GCG GCA TCC ACA GGA GTG Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val 530 535 540	1632
50	GGA GGC CAA GTT AGT GTA AAT ATG CCT CTT CAG AAA ACT ATG GAA ATA Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile 545 550 555 560	1680
	GGG GAG AAC TTA ACA TCT AGA ACA TTT AGA TAT ACC GAT TTT AGT AAT Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn 565 570 575	1728
	CCT TTT TCA TTT AGA GCT AAT CCA GAT ATA ATT GGG ATA AGT GAA CAA Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln 580 585 590	1776

	CCT CTA TTT GGT GCA GGT TCT ATT AGT AGC GGT GAA CTT TAT ATA GAT Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp 595 600 605	1824
5	AAA ATT GAA ATT ATT CTA GCA GAT GCA ACA TTT GAA GCA GAA TCT GAT Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp 610 615 620	1872
10	TTA GAA AGA GCA CAA AAG GCG GTG AAT GCC CTG TTT ACT TCT TCC AAT Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn 625 630 635 640	1920
15	CAA ATC GGG TTA AAA ACC GAT GTG ACG GAT TAT CAT ATT GAT CAA GTA Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val 645 650 655	1968
20	TCC AAT TTA GTG GAT TGT TTA TCA GAT GAA TTT TGT CTG GAT GAA AAG Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys 660 665 670	2016
25	CGA GAA TTG TCC GAG AAA GTC AAA CAT GCG AAG CGA CTC AGT GAT GAG Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu 675 680 685	2064
30	CGG AAT TTA CTT CAA GAT CCA AAC TTC AGA GGG ATC AAT AGA CAA CCA Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro 690 695 700	2112
35	GAC CGT GGC TGG AGA GGA AGT ACA GAT ATT ACC ATC CAA GGA GGA GAT Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp 705 710 715 720	2160
40	GAC GTA TTC AAA GAG AAT TAC GTC ACA CTA CCG GGT ACC GTT GAT GAG Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu 725 730 735	2208
45	TGC TAT CCA ACG TAT TTA TAT CAG AAA ATA GAT GAG TCG AAA TTA AAA Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys 740 745 750	2256
50	GCT TAT ACC CGT TAT GAA TTA AGA GGG TAT ATC GAA GAT AGT CAA GAC Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp 755 760 765	2304
	TTA GAA ATC TAT TTG ATC CGT TAC AAT GCA AAA CAC GAA ATA GTA AAT Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn 770 775 780	2352
	GTG CCA GGC ACG GGT TCC TTA TGG CCG CTT TCA GCC CAA AGT CCA ATC Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile 785 790 795 800	2400

	GGA AAG TGT GGA GAA CCG AAT CGA TGC GCG CCA CAC CTT GAA TGG AAT Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn 805 810 815	2448
5	CCT GAT CTA GAT TGT TCC TGC AGA GAC GGG GAA AAA TGT GCA CAT CAT Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His 820 825 830	2496
10	TCC CAT CAT TTC ACC TTG GAT ATT GAT GTT GGA TGT ACA GAC TTA AAT Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn 835 840 845	2544
15	GAG GAC TTA GGT GTA TGG GTG ATA TTC AAG ATT AAG ACG CAA GAT GGC Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly 850 855 860	2592
20	CAT GCA AGA CTA GGG AAT CTA GAG TTT CTC GAA GAG AAA CCA TTA TTA His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Lys Pro Leu Leu 865 870 875 880	2640
25	GGG GAA GCA CTA GCT CGT GTG AAA AGA GCG GAG AAG AAG TGG AGA GAC Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp 885 890 895	2688
30	AAA CGA GAG AAA CTG CAG TTG GAA ACA AAT ATT GTT TAT AAA GAG GCA Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala 900 905 910	2736
35	AAA GAA TCT GTA GAT GCT TTA TTT GTA AAC TCT CAA TAT GAT AGA TTA Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu 915 920 925	2784
40	CAA GTG GAT ACG AAC ATC GCA ATG ATT CAT GCG GCA GAT AAA CGC GTT Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val 930 935 940	2832
45	CAT AGA ATC CGG GAA GCG TAT CTG CCA GAG TTG TCT GTG ATT CCA GGT His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly 945 950 955 960	2880
50	GTC AAT GCG GCC ATT TTC GAA GAA TTA GAG GGA CGT ATT TTT ACA GCG Val Asn Ala Ala Ile Phe Glu Leu Glu Gly Arg Ile Phe Thr Ala 965 970 975	2928
	TAT TCC TTA TAT GAT GCG AGA AAT GTC ATT AAA AAT GGC GAT TTC AAT Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn 980 985 990	2976
	AAT GGC TTA TTA TGC TGG AAC GTG AAA GGT CAT GTA GAT GTA GAA GAG Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu 995 1000 1005	3024

	CAA AAC AAC CAC CGT TCG GTC CTT GTT ATC CCA GAA TGG GAG GCA GAA Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu 1010	1015	1020	3072
5	GTG TCA CAA GAG GTT CGT GTC TGT CCA GGT CGT GGC TAT ATC CTT CGT Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg 1025	1030	1035	1040
10	GTC ACA GCA TAT AAA GAG GGA TAT GGA GAG GGC TGC GTA ACG ATC CAT Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His 1045	1050	1055	3168
15	GAG ATC GAA GAC AAT ACA GAC GAA CTG AAA TTC AGC AAC TGT GTA GAA Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu 1060	1065	1070	3216
20	GAG GAA GTA TAT CCA AAC ACA GCA GTA ACG TGT AAT AAT TAT ACT GGG Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly 1075	1080	1085	3264
25	ACT CAA GAA GAA TAT GAG GGT ACG TAC ACT TCT CGT AAT CAA GGA TAT Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr 1090	1095	1100	3312
30	GAC GAA GCC TAT GGT AAT AAC CCT TCC GTA CCA GCT GAT TAC GCT TCA Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser 1105	1110	1115	3360
35	GTC TAT GAA GAA AAA TCG TAT ACA GAT GGA CGA AGA GAG AAT CCT TGT Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys 1125	1130	1135	3408
40	GAA TCT AAC AGA GGC TAT GGG GAT TAC ACA CCA CTA CCG GCT GGT TAT Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr 1140	1145	1150	3456
45	GTA ACA AAG GAT TTA GAG TAC TTC CCA GAG ACC GAT AAG GTA TGG ATT Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile 1155	1160	1165	3504
	GAG ATC GGA GAA ACA GAA GGA ACA TTC ATC GTG GAT AGC GTG GAA TTA Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu 1170	1175	1180	3552
	CTC CTT ATG GAG GAA Leu Leu Met Glu Glu 1185			3567

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1189 amino acids
 - (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
1 5 10 15

10 Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn
20 25 30

Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn
35 40 45

15 Phe Val Pro Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp
50 55 60

Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu
65 70 75 80

Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile
85 90 95

20 Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala
100 105 110

Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg
115 120 125

25 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile
130 135 140

30 Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr
145 150 155 160

35 Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile
165 170 175

40 Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr
180 185 190

45 Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn
195 200 205

50 Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp
210 215 220

Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu
225 230 235 240

Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile
245 250 255

	Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile		
	260	265	270
5	Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn		
	275	280	285
	Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu		
	290	295	300
10	Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe		
	305	310	315
	Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Asn		
	325	330	335
15	Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg		
	340	345	350
20	Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr		
	355	360	365
25	Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg		
	370	375	380
	Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr		
	385	390	395
	Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp		
	405	410	415
30	Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala		
	420	425	430
	Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val		
35	435	440	445
	Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro		
	450	455	460
40	Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly		
	465	470	475
	Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu		
	485	490	495
45	Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn		
	500	505	510
	Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser		
50	515	520	525
	Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val		
	530	535	540

Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile
545 550 555 560

5 Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn
565 570 575

Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln
580 585 590

10 Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp
595 600 605

Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp
610 615 620

15 Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn
625 630 635 640

Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val
20 645 650 655

Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys
660 665 670

25 Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu
675 680 685

Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro
690 695 700

30 Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp
705 710 715 720

Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu
35 725 730 735

Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys
740 745 750

40 Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp
755 760 765

Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn
770 775 780

45 Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile
785 790 795 800

Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn
50 805 810 815

Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His
820 825 830

Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn
 835 840 845

5 Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly
 850 855 860

His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu
 865 870 875 880

10 Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp
 885 890 895

Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala
 900 905 910

15 Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu
 915 920 925

Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val
 20 930 935 940

His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly
 945 950 955 960

25 Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala
 965 970 975

Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn
 30 980 985 990

Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu
 995 1000 1005

35 Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu
 1010 1015 1020

Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg
 40 1025 1030 1035 1040

Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His
 1045 1050 1055

Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu
 45 1060 1065 1070

Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly
 1075 1080 1085

50 Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr
 1090 1095 1100

Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser
 1105 1110 1115 1120

Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys
 1125 1130 1135
 5 Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
 1140 1145 1150
 Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile
 1155 1160 1165
 10 Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
 1170 1175 1180
 Leu Leu Met Glu Glu
 1185
 15

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 3567 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 25 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..3567
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
 ATG GAG GAA AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT 48
 Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
 1 5 10 15
 35 AAT CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA ACT GGT AAT 96
 Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn
 20 25 30
 40 TCA TCA ATT GAT ATT TCT CTG TCA CTT GTT CAG TTT CTG GTA TCT AAC 144
 Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn
 35 40 45
 45 TTT GTA CCA GGG GGA GGA TTT TTA GTT GGA TTA ATA GAT TTT GTA TGG 192
 Phe Val Pro Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp
 50 55 60
 50 GGA ATA GTT GGC CCT TCT CAA TGG GAT GCA TTT CTA GTA CAA ATT GAA 240
 Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu
 65 70 75 80
 CAA TTA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT GCT ATT 288
 Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile
 85 90 95

	GCT AAT TTA GAA GGA TTA GGA AAC AAT TTC AAT ATA TAT GTG GAA GCA Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala 100 105 110	336
5	TTT AAA GAA TGG GAA GAA GAT CCT AAT AAT CCA GCA ACC AGG ACC AGA Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg 115 120 125	384
10	GTA ATT GAT CGC TTT CGT ATA CTT GAT GGG CTA CTT GAA AGG GAC ATT Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile 130 135 140	432
15	CCT TCG TTT GAC ATT TCT GGA TTT GAA GTA CCC CTT TTA TCC GTT TAT Pro Ser Phe Asp Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr 145 150 155 160	480
20	GCT CAA GCG GCC AAT CTG CAT CTA GCT ATA TTA AGA GAT TCT GTA ATT Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile 165 170 175	528
25	TTT GGA GAA AGA TGG GGA TTG ACA ACG ATA AAT GTC AAT GAA AAC TAT Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr 180 185 190	576
30	AAT AGA CTA ATT AGG CAT ATT GAT GAA TAT GCT GAT CAC TGT GCA AAT Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn 195 200 205	624
35	ACG TAT AAT CGG GGA TTA AAT AAT TTA CCG AAA TCT ACG TAT CAA GAT Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp 210 215 220	672
40	TGG ATA ACA TAT AAT CGA TTA CGG AGA GAC TTA ACA TTG ACT GTA TTA Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu 225 230 235 240	720
45	GAT ATC GCC GCT TTC TTT CCA AAC TAT GAC AAT AGG AGA TAT CCA ATT Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile 245 250 255	768
50	CAG CCA GTT GGT CAA CTA ACA AGG GAA GTT TAT ACG GAC CCA TTA ATT Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile 260 265 270	816
	AAT TTT AAT CCA CAG TTA CAG TCT GTA GCT CAA TTA CCT ACT TTT AAC Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn 275 280 285	864
	GTT ATG GAG AGC AGC GCA ATT AGA AAT CCT CAT TTA TTT GAT ATA TTG Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu 290 295 300	912

	AAT AAT CTT ACA ATC TTT ACG GAT TGG TTT AGT GTT GGA CGC AAT TTT Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe 305 310 315 320	960
5	TAT TGG GGA GGA CAT CGA GTA ATA TCT AGC CTT ATA GGA GGT GGT AAC Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Asn 325 330 335	1008
10	ATA ACA TCT CCT ATA TAT GGA AGA GAG GCG AAC CAG GAG CCT CCA AGA Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg 340 345 350	1056
15	TCC TTT ACT TTT AAT GGA CCG GTA TTT AGG ACT TTA TCA AAT CCT ACT Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr 355 360 365	1104
20	TTA CGA TTA TTA CAG CAA CCT TGG CCA GCG CCA CCA TTT AAT TTA CGT Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg 370 375 380	1152
25	GGT GTT GAA GGA GTA GAA TTT TCT ACA CCT ACA AAT AGC TTT ACG TAT Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr 385 390 395 400	1200
30	CGA GGA AGA GGT ACG GTT GAT TCT TTA ACT GAA TTA CCG CCT GAG GAT Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp 405 410 415	1248
35	AAT AGT GTG CCA CCT CGC GAA GGA TAT AGT CAT CGT TTA TGT CAT GCA Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala 420 425 430	1296
40	ACT TTT GTT CAA AGA TCT GGA ACA CCT TTT TTA ACA ACT GGT GTA GTA Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val 435 440 445	1344
45	TTT TCT TGG ACG CAT CGT AGT GCA ACT CTT ACA AAT ACA ATT GAT CCA Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro 450 455 460	1392
50	GAG AGA ATT AAT CAA ATA CCT TTA GTG AAA GGA TTT AGA GTT TGG GGG Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly 465 470 475 480	1440
55	GGC ACC TCT GTC ATT ACA GGA CCA GGA TTT ACA GGA GGG GAT ATC CTT Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu 485 490 495	1488
60	CGA AGA AAT ACC TTT GGT GAT TTT GTA TCT CTA CAA GTC AAT ATT AAT Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn 500 505 510	1536

	TCA CCA ATT ACC CAA AGA TAC CGT TTA AGA TTT CGT TAC GCT TCC AGT Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser	515	520	525	1584
5	AGG GAT GCA CGA GTT ATA GTA TTA ACA GGA GCG GCA TCC ACA GGA GTG Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val	530	535	540	1632
10	GGA GGC CAA GTT AGT GTA AAT ATG CCT CTT CAG AAA ACT ATG GAA ATA Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile	545	550	555	1680
15	GGG GAG AAC TTA ACA TCT AGA ACA TTT AGA TAT ACC GAT TTT AGT AAT Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn	565	570	575	1728
20	CCT TTT TCA TTT AGA GCT AAT CCA GAT ATA ATT GGG ATA AGT GAA CAA Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln	580	585	590	1776
25	CCT CTA TTT GGT GCA GGT TCT ATT AGT AGC GGT GAA CTT TAT ATA GAT Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp	595	600	605	1824
30	AAA ATT GAA ATT ATT CTA GCA GAT GCA ACA TTT GAA GCA GAA TCT GAT Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp	610	615	620	1872
35	TTA GAA AGA GCA CAA AAG GCG GTG AAT GCC CTG TTT ACT TCT TCC AAT Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn	625	630	635	1920
40	CAA ATC GGG TTA AAA ACC GAT GTG ACG GAT TAT CAT ATT GAT CAA GTA Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val	645	650	655	1968
45	TCC AAT TTA GTG GAT TGT TTA TCA GAT GAA TTT TGT CTG GAT GAA AAG Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys	660	665	670	2016
50	CGA GAA TTG TCC GAG AAA GTC AAA CAT GCG AAG CGA CTC AGT GAT GAG Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu	675	680	685	2064
55	CGG AAT TTA CTT CAA GAT CCA AAC TTC AGA GGG ATC AAT AGA CAA CCA Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro	690	695	700	2112
60	GAC CGT GGC TGG AGA GGA AGT ACA GAT ATT ACC ATC CAA GGA GGA GAT Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp	705	710	715	2160
					720

	GAC GTA TTC AAA GAG AAT TAC GTC ACA CTA CCG GGT ACC GTT GAT GAG Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu 725 730 735	2208
5	TGC TAT CCA ACG TAT TTA TAT CAG AAA ATA GAT GAG TCG AAA TTA AAA Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys 740 745 750	2256
10	GCT TAT ACC CGT TAT GAA TTA AGA GGG TAT ATC GAA GAT AGT CAA GAC Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp 755 760 765	2304
15	TTA GAA ATC TAT TTG ATC CGT TAC AAT GCA AAA CAC GAA ATA GTA AAT Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn 770 775 780	2352
20	GTG CCA GGC ACG GGT TCC TTA TGG CCG CTT TCA GCC CAA AGT CCA ATC Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile 785 790 795 800	2400
25	GGA AAG TGT GGA GAA CCG AAT CGA TGC GCG CCA CAC CTT GAA TGG AAT Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn 805 810 815	2448
30	CCT GAT CTA GAT TGT TCC TGC AGA GAC GGG GAA AAA TGT GCA CAT CAT Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His 820 825 830	2496
35	TCC CAT CAT TTC ACC TTG GAT ATT GAT GTT GGA TGT ACA GAC TTA AAT Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn 835 840 845	2544
40	GAG GAC TTA GGT GTA TGG GTG ATA TTC AAG ATT AAG ACG CAA GAT GGC Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly 850 855 860	2592
45	CAT GCA AGA CTA GGG AAT CTA GAG TTT CTC GAA GAG AAA CCA TTA TTA His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu 865 870 875 880	2640
50	GGG GAA GCA CTA GCT CGT GTG AAA AGA GCG GAG AAG AAG TGG AGA GAC Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp 885 890 895	2688
	AAA CGA GAG AAA CTG CAG TTG GAA ACA AAT ATT GTT TAT AAA GAG GCA Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala 900 905 910	2736
	AAA GAA TCT GTA GAT GCT TTA TTT GTA AAC TCT CAA TAT GAT AGA TTA Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu 915 920 925	2784

	CAA GTG GAT ACG AAC ATC GCA ATG ATT CAT GCG GCA GAT AAA CGC GTT Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val	930	935	940	2832
5	CAT AGA ATC CGG GAA GCG TAT CTG CCA GAG TTG TCT GTG ATT CCA GGT His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly	945	950	955	2880
10	GTC AAT GCG GCC ATT TTC GAA GAA TTA GAG GGA CGT ATT TTT ACA GCG Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Arg Ile Phe Thr Ala	965	970	975	2928
15	TAT TCC TTA TAT GAT GCG AGA AAT GTC ATT AAA AAT GGC GAT TTC AAT Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn	980	985	990	2976
20	AAT GGC TTA TTA TGC TGG AAC GTG AAA GGT CAT GTA GAT GTA GAA GAG Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu	995	1000	1005	3024
25	CAA AAC AAC CAC CGT TCG GTC CTT GTT ATC CCA GAA TGG GAG GCA GAA Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu	1010	1015	1020	3072
30	GTG TCA CAA GAG GTT CGT GTC TGT CCA GGT CGT GGC TAT ATC CTT CGT Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg	1025	1030	1035	3120
35	GTC ACA GCA TAT AAA GAG GGA TAT GGA GAG GGC TGC GTA ACG ATC CAT Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His	1045	1050	1055	3168
40	GAG ATC GAA GAC AAT ACA GAC GAA CTG AAA TTC AGC AAC TGT GTA GAA Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu	1060	1065	1070	3216
45	GAG GAA GTA TAT CCA AAC AAC ACA GTA ACG TGT AAT AAT TAT ACT GGG Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly	1075	1080	1085	3264
50	ACT CAA GAA GAA TAT GAG GGT ACG TAC ACT TCT CGT AAT CAA GGA TAT Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr	1090	1095	1100	3312
55	GAC GAA GCC TAT GGT AAT AAC CCT TCC GTA CCA GCT GAT TAC GCT TCA Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser	1105	1110	1115	3360
60	GTC TAT GAA GAA AAA TCG TAT ACA GAT GGA CGA AGA GAG AAT CCT TGT Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys	1125	1130	1135	3408

GAA TCT AAC AGA GGC TAT GGG GAT TAC ACA CCA CTA CCG GCT GGT TAT	3456	
Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr		
1140	1145	1150
5 GTA ACA AAG GAT TTA GAG TAC TTC CCA GAG ACC GAT AAG GTA TGG ATT	3504	
Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile		
1155	1160	1165
10 GAG ATC GGA GAA ACA GAA GGA ACA TTC ATC GTG GAT AGC GTG GAA TTA	3552	
Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu		
1170	1175	1180
15 CTC CTT ATG GAG GAA	3567	
Leu Leu Met Glu Glu		
1185		

(2) INFORMATION FOR SEQ ID NO:4:

Pro Ser Phe Asp Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr
 145 150 155 160

5 Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile
 165 170 175

Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr
 180 185 190

10 Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn
 195 200 205

Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp
 15 210 215 220

Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu
 225 230 235 240

20 Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile
 245 250 255

Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile
 260 265 270

25 Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn
 275 280 285

Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu
 30 290 295 300

Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe
 305 310 315 320

35 Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Asn
 325 330 335

Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg
 40 340 345 350

Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr
 355 360 365

Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg
 45 370 375 380

Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr
 385 390 395 400

50 Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp
 405 410 415

Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala
 420 425 430

Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val
 435 440 445

5 Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro
 450 455 460

Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly
 465 470 475 480

10 Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu
 485 490 495

Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn -
 15 500 505 510

Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser
 515 520 525

20 Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val
 530 535 540

Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile
 545 550 555 560

25 Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn
 565 570 575

Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln
 30 580 585 590

Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp
 595 600 605

35 Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp
 610 615 620

Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn
 625 630 635 640

40 Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val
 645 650 655

Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys
 45 660 665 670

Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu
 675 680 685

50 Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro
 690 695 700

Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp
 705 710 715 720

	Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu			
	725	730	735	
5	Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys			
	740	745	750	
	Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp			
	755	760	765	
10	Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn			
	770	775	780	
15	Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile			
	785	790	795	800
	Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn			
	805	810	815	
20	Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His			
	820	825	830	
	Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn			
	835	840	845	
25	Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly			
	850	855	860	
30	His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu			
	865	870	875	880
35	Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp			
	885	890	895	
	Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala			
	900	905	910	
	Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu			
	915	920	925	
40	Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val			
	930	935	940	
	His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly			
45	945	950	955	960
	Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala			
	965	970	975	
50	Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn			
	980	985	990	
	Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu			
	995	1000	1005	

Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu
1010 1015 1020

5 Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg
1025 1030 1035 1040

Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His
1045 1050 1055

10 Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu
1060 1065 1070

Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly
15 1075 1080 1085

Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr
1090 1095 1100

20 Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser
1105 1110 1115 1120

Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys
1125 1130 1135

25 Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
1140 1145 1150

Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile
30 1155 1160 1165

Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
1170 1175 1180

35 Leu Leu Met Glu Glu
1185

(2) INFORMATION FOR SEQ ID NO:5:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3567

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

	ATG GAG GAA AAT AAT CAA	AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT	48
	Met Glu Glu Asn Asn Gln	Gln Cys Ile Pro Tyr Asn Cys Leu Ser	
	1	5	10
			15
5	AAT CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA ACT GGT AAT		96
	Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn		
	20	25	30
10	TCA TCA ATT GAT ATT TCT CTG TCA CTT GTT CAG TTT CTG GTA TCT AAC		144
	Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn		
	35	40	45
15	TTT GTA CCA GGG GGA GGA TTT TTA GTT GGA TTA ATA GAT TTT GTA TGG		192
	Phe Val Pro Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp		
	50	55	60
20	GGA ATA GTT GGC CCT TCT CAA TGG GAT GCA TTT CTA GTA CAA ATT GAA		240
	Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu		
	65	70	75
			80
25	CAA TTA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT GCT ATT		288
	Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile		
	85	90	95
30	GCT AAT TTA GAA GGA TTA GGA AAC AAT TTC AAT ATA TAT GTG GAA GCA		336
	Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala		
	100	105	110
35	TTT AAA GAA TGG GAA GAA GAT CCT AAT AAT CCA GCA ACC AGG ACC AGA		384
	Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg		
	115	120	125
40	GTA ATT GAT CGC TTT CGT ATA CTT GAT GGG CTA CTT GAA AGG GAC ATT		432
	Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile		
	130	135	140
45	CCT TCG TTT CGA ATT TCT GGA TTT GAA GAT CCC CTT TTA TCC GTT TAT		480
	Pro Ser Phe Arg Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr		
	145	150	155
			160
50	GCT CAA GCG GCC AAT CTG CAT CTA GCT ATA TTA AGA GAT TCT GTA ATT		528
	Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile		
	165	170	175
55	TTT GGA GAA GCA TGG GGG TTG ACA ACG ATA AAT GTC AAT GAA AAC TAT		576
	Phe Gly Ala Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr		
	180	185	190
60	AAT AGA CTA ATT AGG CAT ATT GAT GAA TAT GCT GAT CAC TGT GCA AAT		624
	Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn		
	195	200	205

	ACG TAT AAT CGG GGA TTA AAT AAT TTA CCG AAA TCT ACG TAT CAA GAT Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp	210	215	220	672
5	TGG ATA ACA TAT AAT CGA TTA CGG AGA GAC TTA ACA TTG ACT GTA TTA Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu	225	230	235	240
10	GAT ATC GCC GCT TTC TTT CCA AAC TAT GAC AAT AGG AGA TAT CCA ATT Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile	245	250	255	768
15	CAG CCA GTT GGT CAA CTA ACA AGG GAA GTT TAT ACG GAC CCA TTA ATT Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile	260	265	270	816
20	AAT TTT AAT CCA CAG TTA CAG TCT GTA GCT CAA TTA CCT ACT TTT AAC Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn	275	280	285	864
25	GTT ATG GAG AGC AGC GCA ATT AGA AAT CCT CAT TTA TTT GAT ATA TTG Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu	290	295	300	912
30	AAT AAT CTT ACA ATC TTT ACG GAT TGG TTT AGT GTT GGA CGC AAT TTT Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe	305	310	315	960
35	TAT TGG GGA GGA CAT CGA GTA ATA TCT AGC CTT ATA GGA GGT GGT AAC Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Asn	325	330	335	1008
40	ATA ACA TCT ATA TAT GGA AGA GAG GCG AAC CAG GAG CCT CCA AGA Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg	340	345	350	1056
45	TCC TTT ACT TTT AAT GGA CCG GTA TTT AGG ACT TTA TCA AAT CCT ACT Ser Phe Thr Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr	355	360	365	1104
50	TTA CGA TTA TTA CAG CAA CCT TGG CCA GCG CCA CCA TTT AAT TTA CGT Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg	370	375	380	1152
	GGT GTT GAA GGA GTA GAA TTT TCT ACA CCT ACA AAT AGC TTT ACG TAT Gly Val Glu Gly Val Glu Phe Ser Thr Pro Asn Ser Phe Thr Tyr	385	390	395	400
	CGA GGA AGA GGT ACG GTT GAT TCT TTA ACT GAA TTA CCG CCT GAG GAT Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp	405	410	415	1248

	AAT AGT GTG CCA CCT CGC GAA GGA TAT AGT CAT CGT TTA TGT CAT GCA		1296
	Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala		
	420	425	430
5	ACT TTT GTT CAA AGA TCT GGA ACA CCT TTT TTA ACA ACT GGT GTA GTA		1344
	Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val		
	435	440	445
10	TTT TCT TGG ACG CAT CGT AGT GCA ACT CTT ACA AAT ACA ATT GAT CCA		1392
	Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro		
	450	455	460
15	GAG AGA ATT AAT CAA ATA CCT TTA GTG AAA GGA TTT AGA GTT TGG GGG		1440
	Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly		
	465	470	475
	480		
20	GGC ACC TCT GTC ATT ACA GGA CCA GGA TTT ACA GGA GGG GAT ATC CTT		1488
	Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu		
	485	490	495
25	CGA AGA AAT ACC TTT GGT GAT TTT GTA TCT CTA CAA GTC AAT ATT AAT		1536
	Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn		
	500	505	510
30	TCA CCA ATT ACC CAA AGA TAC CGT TTA AGA TTT CGT TAC GCT TCC AGT		1584
	Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser		
	515	520	525
35	AGG GAT GCA CGA GTT ATA GTA TTA ACA GGA GCG GCA TCC ACA GGA GTG		1632
	Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val		
	530	535	540
40	GGA GGC CAA GTT AGT GTA AAT ATG CCT CTT CAG AAA ACT ATG GAA ATA		1680
	Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile		
	545	550	555
	560		
45	GGG GAG AAC TTA ACA TCT AGA ACA TTT AGA TAT ACC GAT TTT AGT AAT		1728
	Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn		
	565	570	575
50	CCT TTT TCA TTT AGA GCT AAT CCA GAT ATA ATT GGG ATA AGT GAA CAA		1776
	Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln		
	580	585	590
	CCT CTA TTT GGT GCA GGT TCT ATT AGT AGC GGT GAA CTT TAT ATA GAT		1824
	Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp		
	595	600	605
55	AAA ATT GAA ATT ATT CTA GCA GAT GCA ACA TTT GAA GCA GAA TCT GAT		1872
	Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp		
	610	615	620

	TTA GAA AGA GCA CAA AAG GCG GTG AAT GCC CTG TTT ACT TCT TCC AAT Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn 625 630 635 640	1920
5	CAA ATC GGG TTA AAA ACC GAT GTG ACG GAT TAT CAT ATT GAT CAA GTA Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val 645 650 655	1968
10	TCC AAT TTA GTG GAT TGT TTA TCA GAT GAA TTT TGT CTG GAT GAA AAG Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys 660 665 670	2016
15	CGA GAA TTG TCC GAG AAA GTC AAA CAT GCG AAG CGA CTC AGT GAT GAG Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu 675 680 685	2064
20	CGG AAT TTA CTT CAA GAT CCA AAC TTC AGA GGG ATC AAT AGA CAA CCA Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro 690 695 700	2112
25	GAC CGT GGC TGG AGA GGA AGT ACA GAT ATT ACC ATC CAA GGA GGA GAT Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp 705 710 715 720	2160
30	GAC GTA TTC AAA GAG AAT TAC GTC ACA CTA CCG GGT ACC GTT GAT GAG Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu 725 730 735	2208
35	TGC TAT CCA ACG TAT TTA TAT CAG AAA ATA GAT GAG TCG AAA TTA AAA Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys 740 745 750	2256
40	GCT TAT ACC CGT TAT GAA TTA AGA GGG TAT ATC GAA GAT AGT CAA GAC Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp 755 760 765	2304
45	TTA GAA ATC TAT TTG ATC CGT TAC AAT GCA AAA CAC GAA ATA GTA AAT Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn 770 775 780	2352
50	GTG CCA GGC ACG GGT TCC TTA TGG CCG CTT TCA GCC CAA AGT CCA ATC Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile 785 790 795 800	2400
	GGA AAG TGT GGA GAA CCG AAT CGA TGC GCG CCA CAC CTT GAA TGG AAT Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn 805 810 815	2448
	CCT GAT CTA GAT TGT TCC TGC AGA GAC GGG GAA AAA TGT GCA CAT CAT Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His 820 825 830	2496

	TCC CAT CAT TTC ACC TTG GAT ATT GAT GTT GGA TGT ACA GAC TTA AAT Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn 835 840 845	2544
5	GAG GAC TTA GGT GTA TGG GTG ATA TTC AAG ATT AAG ACG CAA GAT GGC Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly 850 855 860	2592
10	CAT GCA AGA CTA GGG AAT CTA GAG TTT CTC GAA GAG AAA CCA TTA TTA His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu 865 870 875 880	2640
15	GGG GAA GCA CTA GCT CGT GTG AAA AGA GCG GAG AAG AAG TGG AGA GAC Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp 885 890 895	2688
20	AAA CGA GAG AAA CTG CAG TTG GAA ACA AAT ATT GTT TAT AAA GAG GCA Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala 900 905 910	2736
25	AAA GAA TCT GTA GAT GCT TTA TTT GTA AAC TCT CAA TAT GAT AGA TTA Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu 915 920 925	2784
30	CAA GTG GAT ACG AAC ATC GCA ATG ATT CAT GCG GCA GAT AAA CGC GTT Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val 930 935 940	2832
35	CAT AGA ATC CGG GAA GCG TAT CTG CCA GAG TTG TCT GTG ATT CCA GGT His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly 945 950 955 960	2880
40	GTC AAT GCG GCC ATT TTC GAA GAA TTA GAG GGA CGT ATT TTT ACA GCG Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala 965 970 975	2928
45	TAT TCC TTA TAT GAT GCG AGA AAT GTC ATT AAA AAT GGC GAT TTC AAT Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn 980 985 990	2976
50	AAT GGC TTA TTA TGC TGG AAC GTG AAA GGT CAT GTA GAT GTA GAA GAG Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu 995 1000 1005	3024
55	CAA AAC AAC CAC CGT TCG GTC CTT GTT ATC CCA GAA TGG GAG GCA GAA Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu 1010 1015 1020	3072
60	GTG TCA CAA GAG GTT CGT GTC TGT CCA GGT CGT GGC TAT ATC CTT CGT Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg 1025 1030 1035 1040	3120

Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
 1 5 10 15

	Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn			
	20	25	30	
5	Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn			
	35	40	45	
	Phe Val Pro Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp			
	50	55	60	
10	Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu			
	65	70	75	80
15	Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile			
	85	90	95	
	Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala			
	100	105	110	
20	Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg			
	115	120	125	
25	Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile			
	130	135	140	
30	Pro Ser Phe Arg Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr			
	145	150	155	160
35	Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile			
	165	170	175	
40	Phe Gly Glu Ala Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr			
	180	185	190	
45	Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn			
	195	200	205	
50	Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp			
	210	215	220	
	Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu			
	225	230	235	240
	Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile			
	245	250	255	
	Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile			
	260	265	270	
	Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn			
	275	280	285	
	Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu			
	290	295	300	

	Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe		
	305	310	315
	320		
5	Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Asn		
	325	330	335
	Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg		
	340	345	350
10	Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr		
	355	360	365
	Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg		
15	370	375	380
	Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr		
	385	390	395
	400		
20	Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp		
	405	410	415
	Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala		
	420	425	430
25	Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val		
	435	440	445
30	Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro		
	450	455	460
35	Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly		
	465	470	475
	480		
40	Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu		
	485	490	495
	Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn		
	500	505	510
	515	520	525
45	Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val		
	530	535	540
	545	550	555
	560		
50	Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn		
	565	570	575
	Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln		
	580	585	590

Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp
 595 600 605

5 Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp
 610 615 620

Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn
 625 630 635 640

10 Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val
 645 650 655

Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys
 15 660 665 670

Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu
 675 680 685

20 Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro
 690 695 700

Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp
 705 710 715 720

25 Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu
 725 730 735

Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys
 30 740 745 750

Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp
 755 760 765

35 Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn
 770 775 780

Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile
 40 785 790 795 800

Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn
 805 810 815

45 Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His
 820 825 830

Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn
 835 840 845

50 Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly
 850 855 860

His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Lys Pro Leu Leu
 865 870 875 880

Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp
 885 890 895

5 Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala
 900 905 910

Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu
 915 920 925

10 Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val
 930 935 940

His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly
 15 945 950 955 960

Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala
 965 970 975

20 Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn
 980 985 990

Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu
 995 1000 1005

25 Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu
 1010 1015 1020

Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg
 1025 1030 1035 1040

30 Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His
 1045 1050 1055

Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu
 35 1060 1065 1070

Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly
 1075 1080 1085

40 Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr
 1090 1095 1100

Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser
 45 1105 1110 1115 1120

Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys
 1125 1130 1135

50 Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
 1140 1145 1150

Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile
 1155 1160 1165

Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
1170 1175 1180

5 Leu Leu Met Glu Glu
1185

(2) INFORMATION FOR SEQ ID NO:7:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3567

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG GAG GAA AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT
Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
1 5 10 15

48

AAT CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA ACT GGT AAT
Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn
20 25 30

96

TCA TCA ATT GAT ATT TCT CTG TCA CTT GTT CAG TTT CTG GTA TCT AAC
Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn
35 40 45

144

TTT GTA CCA GGG GGA GGA TTT TTA GTT GGA TTA ATA GAT TTT GTA TGG
Phe Val Pro Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp
50 55 60

192

40

GGA ATA GTT GGC CCT TCT CAA TGG GAT GCA TTT CTA GTA CAA ATT GAA
Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu
65 70 75 80

240

45

CAA TTA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT GCT ATT
Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile
85 90 95

288

50

GCT AAT TTA GAA GGA TTA GGA AAC AAT TTC AAT ATA TAT GTG GAA GCA
Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala
100 105 110

336

TTT AAA GAA TGG GAA GAT GAT CCT CAT AAT CCC ACA ACC AGG ACC AGA
Phe Lys Glu Trp Glu Asp Asp Pro His Asn Pro Thr Thr Arg Thr Arg
115 120 125

384

	GTA ATT GAT CGC TTT CGT ATA CTT GAT GGG CTA CTT GAA AGG GAC ATT Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile 130 135 140	432
5	CCT TCG TTT CGA ATT TCT GGA TTT GAA GTA CCC CTT TTA TCC GTT TAT Pro Ser Phe Arg Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr 145 150 155 160	480
10	GCT CAA GCG GCC AAT CTG CAT CTA GCT ATA TTA AGA GAT TCT GTA ATT Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile 165 170 175	528
15	TTT GGA GAA AGA TGG GGA TTG ACA ACG ATA AAT GTC AAT GAA AAC TAT Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr 180 185 190	576
20	AAT AGA CTA ATT AGG CAT ATT GAT GAA TAT GCT GAT CAC TGT GCA AAT Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn 195 200 205	624
25	ACG TAT AAT CGG GGA TTA AAT AAT TTA CCG AAA TCT ACG TAT CAA GAT Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp 210 215 220	672
30	TGG ATA ACA TAT AAT CGA TTA CGG AGA GAC TTA ACA TTG ACT GTA TTA Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu 225 230 235 240	720
35	GAT ATC GCC GCT TTC TTT CCA AAC TAT GAC AAT AGG AGA TAT CCA ATT Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile 245 250 255	768
40	CAG CCA GTT GGT CAA CTA ACA AGG GAA GTT TAT ACG GAC CCA TTA ATT Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile 260 265 270	816
45	AAT TTT AAT CCA CAG TTA CAG TCT GTA GCT CAA TTA CCT ACT TTT AAC Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn 275 280 285	864
50	GTT ATG GAG AGC AGC GCA ATT AGA AAT CCT CAT TTA TTT GAT ATA TTG Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu 290 295 300	912
	AAT AAT CTT ACA ATC TTT ACG GAT TGG TTT AGT GTT GGA CGC AAT TTT Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe 305 310 315 320	960
	TAT TGG GGA GGA CAT CGA GTA ATA TCT AGC CTT ATA GGA GGT GGT AAC Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Asn 325 330 335	1008

	ATA ACA TCT CCT ATA TAT [*] GGA AGA GAG GCG AAC CAG GAG CCT CCA AGA Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg 340	345	350	1056
5	TCC TTT ACT TTT AAT GGA CCG GTA TTT AGG ACT TTA TCA AAT CCT ACT Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr 355	360	365	1104
10	TTA CGA TTA TTA CAG CAA CCT TGG CCA GCG CCA CCA TTT AAT TTA CGT Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg 370	375	380	1152
15	GGT GTT GAA GGA GTA GAA TTT TCT ACA CCT ACA AAT AGC TTT ACG TAT Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr 385	390	395	1200
20	CGA GGA AGA GGT ACG GTT GAT TCT TTA ACT GAA TTA CCG CCT GAG GAT Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp 405	410	415	1248
25	AAT AGT GTG CCA CCT CGC GAA GGA TAT AGT CAT CGT TTA TGT CAT GCA Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala 420	425	430	1296
30	ACT TTT GTT CAA AGA TCT GGA ACA CCT TTT TTA ACA ACT GGT GTA GTA Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val 435	440	445	1344
35	TTT TCT TGG ACG CAT CGT AGT GCA ACT CTT ACA AAT ACA ATT GAT CCA Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro 450	455	460	1392
40	GAG AGA ATT AAT CAA ATA CCT TTA GTG AAA GGA TTT AGA GTT TGG GGG Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly 465	470	475	1440
45	GGC ACC TCT GTC ATT ACA GGA CCA GGA TTT ACA GGA GGG GAT ATC CTT Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu 485	490	495	1488
50	CGA AGA AAT ACC TTT GGT GAT TTT GTA TCT CTA CAA GTC AAT ATT AAT Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn 500	505	510	1536
55	TCA CCA ATT ACC CAA AGA TAC CGT TTA AGA TTT CGT TAC GCT TCC AGT Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser 515	520	525	1584
60	AGG GAT GCA CGA GTT ATA GTA TTA ACA GGA GCG GCA TCC ACA GGA GTG Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val 530	535	540	1632

	GGA GGC CAA GTT AGT GTA AAT ATG CCT CTT CAG AAA ACT ATG GAA ATA Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile 545 550 555 560	1680
5	GGG GAG AAC TTA ACA TCT AGA ACA TTT AGA TAT ACC GAT TTT AGT AAT Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn 565 570 575	1728
10	CCT TTT TCA TTT AGA GCT AAT CCA GAT ATA ATT GGG ATA AGT GAA CAA Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln 580 585 590	1776
15	CCT CTA TTT GGT GCA GGT TCT ATT AGT AGC GGT GAA CTT TAT ATA GAT Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp 595 600 605	1824
20	AAA ATT GAA ATT ATT CTA GCA GAT GCA ACA TTT GAA GCA GAA TCT GAT Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp 610 615 620	1872
25	TTA GAA AGA GCA CAA AAG GCG GTG AAT GCC CTG TTT ACT TCT TCC AAT Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn 625 630 635 640	1920
30	CAA ATC GGG TTA AAA ACC GAT GTG ACG GAT TAT CAT ATT GAT CAA GTA Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val 645 650 655	1968
35	TCC AAT TTA GTG GAT TGT TTA TCA GAT GAA TTT TGT CTG GAT GAA AAG Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys 660 665 670	2016
40	CGA GAA TTG TCC GAG AAA GTC AAA CAT GCG AAG CGA CTC AGT GAT GAG Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu 675 680 685	2064
45	CGG AAT TTA CTT CAA GAT CCA AAC TTC AGA GGG ATC AAT AGA CAA CCA Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro 690 695 700	2112
50	GAC CGT GGC TGG AGA GGA AGT ACA GAT ATT ACC ATC CAA GGA GGA GAT Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp 705 710 715 720	2160
	GAC GTA TTC AAA GAG AAT TAC GTC ACA CTA CCG GGT ACC GTT GAT GAG Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu 725 730 735	2208
	TGC TAT CCA ACG TAT TTA TAT CAG AAA ATA GAT GAG TCG AAA TTA AAA Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys 740 745 750	2256

	GCT TAT ACC CGT TAT GAA TTA AGA GGG TAT ATC GAA GAT AGT CAA GAC Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp	755	760	765	2304
5	TTA GAA ATC TAT TTG ATC CGT TAC AAT GCA AAA CAC GAA ATA GTA AAT Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn	770	775	780	2352
10	GTG CCA GGC ACG GGT TCC TTA TGG CCG CTT TCA GCC CAA AGT CCA ATC Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile	785	790	795	2400
15	GGA AAG TGT GGA GAA CCG AAT CGA TGC GCG CCA CAC CTT GAA TGG AAT Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn	805	810	815	2448
20	CCT GAT CTA GAT TGT TCC TGC AGA GAC GGG GAA AAA TGT GCA CAT CAT Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His	820	825	830	2496
25	TCC CAT CAT TTC ACC TTG GAT ATT GAT GTT GGA TGT ACA GAC TTA AAT Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn	835	840	845	2544
30	GAG GAC TTA GGT GTA TGG GTG ATA TTC AAG ATT AAG ACG CAA GAT GGC Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly	850	855	860	2592
35	CAT GCA AGA CTA GGG AAT CTA GAG TTT CTC GAA GAG AAA CCA TTA TTA His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu	865	870	875	2640
40	GGG GAA GCA CTA GCT CGT GTG AAA AGA GCG GAG AAG AAG TGG AGA GAC Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp	885	890	895	2688
45	AAA CGA GAG AAA CTG CAG TTG GAA ACA AAT ATT GTT TAT AAA GAG GCA Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala	900	905	910	2736
50	AAA GAA TCT GTA GAT GCT TTA TTT GTA AAC TCT CAA TAT GAT AGA TTA Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu	915	920	925	2784
	CAA GTG GAT ACG AAC ATC GCA ATG ATT CAT GCG GCA GAT AAA CGC GTT Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val	930	935	940	2832
	CAT AGA ATC CGG GAA GCG TAT CTG CCA GAG TTG TCT GTG ATT CCA GGT His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly	945	950	955	2880
					960

	GTC AAT GCG GCC ATT TTC GAA GAA TTA GAG GGA CGT ATT TTT ACA GCG	2928
	Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala	
	965 970 975	
5	TAT TCC TTA TAT GAT GCG AGA AAT GTC ATT AAA AAT GGC GAT TTC AAT	2976
	Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn	
	980 985 990	
10	AAT GGC TTA TTA TGC TGG AAC GTG AAA GGT CAT GTA GAT GTA GAA GAG	3024
	Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu	
	995 1000 1005	
15	CAA AAC AAC CAC CGT TCG GTC CTT GTT ATC CCA GAA TGG GAG GCA GAA	3072
	Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu	
	1010 1015 1020	
20	GTG TCA CAA GAG GTT CGT GTC TGT CCA GGT CGT GGC TAT ATC CTT CGT	3120
	Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg	
	1025 1030 1035 1040	
25	GTC ACA GCA TAT AAA GAG GGA TAT GGA GAG GGC TGC GTA ACG ATC CAT	3168
	Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His	
	1045 1050 1055	
30	GAG ATC GAA GAC AAT ACA GAC GAA CTG AAA TTC AGC AAC TGT GTA GAA	3216
	Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu	
	1060 1065 1070	
35	GAG GAA GTA TAT CCA AAC AAC ACA GTA ACG TGT AAT AAT TAT ACT GGG	3264
	Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly	
	1075 1080 1085	
40	ACT CAA GAA GAA TAT GAG GGT ACG TAC ACT TCT CGT AAT CAA GGA TAT	3312
	Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr	
	1090 1095 1100	
45	GAC GAA GCC TAT GGT AAT AAC CCT TCC GTA CCA GCT GAT TAC GCT TCA	3360
	Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser	
	1105 1110 1115 1120	
50	GTC TAT GAA GAA AAA TCG TAT ACA GAT GGA CGA AGA GAG AAT CCT TGT	3408
	Val Tyr Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys	
	1125 1130 1135	
45	GAA TCT AAC AGA GGC TAT GGG GAT TAC ACA CCA CTA CCG GCT GGT TAT	3456
	Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr	
	1140 1145 1150	
50	GTA ACA AAG GAT TTA GAG TAC TTC CCA GAG ACC GAT AAG GTA TGG ATT	3504
	Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile	
	1155 1160 1165	

GAG ATC GGA GAA ACA GAA GGA ACA TTC ATC GTG GAT AGC GTG GAA TTA 3552
Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
1170 1175 1180

5 CTC CTT ATG GAG GAA 3567
Leu Leu Met Glu Glu
1185

10 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1189 amino acids
 (B) TYPE: amino acid
15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

20 Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
 1 5 10 15

25 Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn
 20 25 30

30 Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn
 35 40 45

35 Phe Val Pro Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp
 50 55 60

40 Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu
 65 70 75 80

45 Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile
 85 90 95

50 Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala
 100 105 110

55 Phe Lys Glu Trp Glu Asp Asp Pro His Asn Pro Thr Thr Arg Thr Arg
 115 120 125

60 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile
 130 135 140

65 Pro Ser Phe Arg Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr
 145 150 155 160

70 Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile
 165 170 175

	Phe	Gly	Glu	Arg	Trp	Gly	Leu	Thr	Thr	Ile	Asn	Val	Asn	Glu	Asn	Tyr
	180						185							190		
5	Asn	Arg	Leu	Ile	Arg	His	Ile	Asp	Glu	Tyr	Ala	Asp	His	Cys	Ala	Asn
	195						200							205		
	Thr	Tyr	Asn	Arg	Gly	Leu	Asn	Asn	Leu	Pro	Lys	Ser	Thr	Tyr	Gln	Asp
	210						215							220		
10	Trp	Ile	Thr	Tyr	Asn	Arg	Leu	Arg	Arg	Asp	Leu	Thr	Leu	Thr	Val	Leu
	225						230							235		240
	Asp	Ile	Ala	Ala	Phe	Phe	Pro	Asn	Tyr	Asp	Asn	Arg	Arg	Tyr	Pro	Ile
	245						250							255		
15	Gln	Pro	Val	Gly	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Ile
	260						265							270		
20	Asn	Phe	Asn	Pro	Gln	Leu	Gln	Ser	Val	Ala	Gln	Leu	Pro	Thr	Phe	Asn
	275						280							285		
25	Val	Met	Glu	Ser	Ser	Ala	Ile	Arg	Asn	Pro	His	Leu	Phe	Asp	Ile	Leu
	290						295							300		
30	Asn	Asn	Leu	Thr	Ile	Phe	Thr	Asp	Trp	Phe	Ser	Val	Gly	Arg	Asn	Phe
	305						310							315		320
35	Tyr	Trp	Gly	Gly	His	Arg	Val	Ile	Ser	Ser	Leu	Ile	Gly	Gly	Asn	
	325						330							335		
40	Ile	Thr	Ser	Pro	Ile	Tyr	Gly	Arg	Glu	Ala	Asn	Gln	Glu	Pro	Pro	Arg
	340						345							350		
45	Ser	Phe	Thr	Phe	Asn	Gly	Pro	Val	Phe	Arg	Thr	Leu	Ser	Asn	Pro	Thr
	355						360							365		
50	Leu	Arg	Leu	Leu	Gln	Gln	Pro	Trp	Pro	Ala	Pro	Pro	Phe	Asn	Leu	Arg
	370						375							380		
	Gly	Val	Glu	Gly	Val	Glu	Phe	Ser	Thr	Pro	Thr	Asn	Ser	Phe	Thr	Tyr
	385						390							395		400
	Arg	Gly	Arg	Gly	Thr	Val	Asp	Ser	Leu	Thr	Glu	Leu	Pro	Pro	Glu	Asp
	405						410							415		
45	Asn	Ser	Val	Pro	Pro	Arg	Glu	Gly	Tyr	Ser	His	Arg	Leu	Cys	His	Ala
	420						425							430		
50	Thr	Phe	Val	Gln	Arg	Ser	Gly	Thr	Pro	Phe	Leu	Thr	Thr	Gly	Val	Val
	435						440							445		
	Phe	Ser	Trp	Thr	His	Arg	Ser	Ala	Thr	Leu	Thr	Asn	Thr	Ile	Asp	Pro
	450						455							460		

	Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly			
	465	470	475	480
	Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu			
5	485	490	495	
	Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn			
	500	505	510	
10	Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser			
	515	520	525	
	Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val			
	530	535	540	
15	Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile			
	545	550	555	560
20	Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn			
	565	570	575	
	Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln			
	580	585	590	
25	Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp			
	595	600	605	
	Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp			
	610	615	620	
30	Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn			
	625	630	635	640
	Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val			
	645	650	655	
	Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys			
	660	665	670	
40	Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu			
	675	680	685	
	Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro			
	690	695	700	
45	Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp			
	705	710	715	720
	Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu			
50	725	730	735	
	Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys			
	740	745	750	

Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His
 1045 1050 1055

5 Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu
 1060 1065 1070

Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly
 1075 1080 1085

10 Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr
 1090 1095 1100

Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser
 1105 1110 1115 1120

15 Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys
 1125 1130 1135

Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
 20 1140 1145 1150

Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile
 1155 1160 1165

25 Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
 1170 1175 1180

Leu Leu Met Glu Glu
 1185

30

(2) INFORMATION FOR SEQ ID NO:9:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3567 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..3567

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
 ATG GAG GAA AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT
 Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
 1 5 10 15

50 AAT CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA ACT GGT AAT
 Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn
 20 25 30

48

96

	TCA TCA ATT GAT ATT TCT CTG TCA CTT GTT CAG TTT CTG GTA TCT AAC Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn	35	40	45	144
5	TTT GTA CCA GGG GGA TTT TTA GTT GGA TTA ATA GAT TTT GTA TGG Phe Val Pro Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp	50	55	60	192
10	GGA ATA GTT GGC CCT TCT CAA TGG GAT GCA TTT CTA GTA CAA ATT GAA Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu	65	70	75	240
15	CAA TTA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT GCT ATT Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile	85	90	95	288
20	GCT AAT TTA GAA GGA TTA GGA AAC AAT TTC AAT ATA TAT GTG GAA GCA Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala	100	105	110	336
25	TTT AAA GAA TGG GAA GTA GAT CCT AAT AAT CCT GGA ACC AGG ACC AGA Phe Lys Glu Trp Glu Val Asp Pro Asn Asn Pro Gly Thr Arg Thr Arg	115	120	125	384
30	GTA ATT GAT CGC TTT CGT ATA CTT GAT GGG CTA CTT GAA AGG GAC ATT Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile	130	135	140	432
35	CCT TCG TTT CGA ATT TCT GGA TTT GAA GTA CCC CTT TTA TCC GTT TAT Pro Ser Phe Arg Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr	145	150	155	480
40	GCT CAA GCG GCC AAT CTG CAT CTA GCT ATA TTA AGA GAT TCT GTA ATT Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile	165	170	175	528
45	TTT GGA GAA AGA TGG GGA TTG ACA ACG ATA AAT GTC AAT GAA AAC TAT Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr	180	185	190	576
50	AAT AGA CTA ATT AGG CAT ATT GAT GAA TAT GCT GAT CAC TGT GCA AAT Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn	195	200	205	624
	ACG TAT AAT CGG GGA TTA AAT AAT TTA CCG AAA TCT ACG TAT CAA GAT Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp	210	215	220	672
	TGG ATA ACA TAT AAT CGA TTA CGG AGA GAC TTA ACA TTG ACT GTA TTA Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu	225	230	235	720
					240

	GAT ATC GCC GCT TTC TTT CCA AAC TAT GAC AAT AGG AGA TAT CCA ATT Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile 245	250	255	768
5	CAG CCA GTT GGT CAA CTA ACA AGG GAA GTT TAT ACG GAC CCA TTA ATT Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile 260	265	270	816
10	AAT TTT AAT CCA CAG TTA CAG TCT GTA GCT CAA TTA CCT ACT TTT AAC Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn 275	280	285	864
15	GTT ATG GAG AGC AGC GCA ATT AGA AAT CCT CAT TTA TTT GAT ATA TTG Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu 290	295	300	912
20	AAT AAT CTT ACA ATC TTT ACG GAT TGG TTT AGT GTT GGA CGC AAT TTT Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe 305	310	315	960
25	TAT TGG GGA GGA CAT CGA GTA ATA TCT AGC CTT ATA GGA GGT GGT AAC Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Asn 325	330	335	1008
30	ATA ACA TCT CCT ATA TAT GGA AGA GAG GCG AAC CAG GAG CCT CCA AGA Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg 340	345	350	1056
35	TCC TTT ACT TTT AAT GGA CCG GTA TTT AGG ACT TTA TCA AAT CCT ACT Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr 355	360	365	1104
40	TTA CGA TTA TTA CAG CAA CCT TGG CCA GCG CCA CCA TTT AAT TTA CGT Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg 370	375	380	1152
45	GGT GTT GAA GGA GTA GAA TTT TCT ACA CCT ACA AAT AGC TTT ACG TAT Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr 385	390	395	400
50	CGA GGA AGA GGT ACG GTT GAT TCT TTA ACT GAA TTA CCG CCT GAG GAT Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp 405	410	415	1248
	AAT AGT GTG CCA CCT CGC GAA GGA TAT AGT CAT CGT TTA TGT CAT GCA Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala 420	425	430	1296
	ACT TTT GTT CAA AGA TCT GGA ACA CCT TTT TTA ACA ACT GGT GTA GTA Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val 435	440	445	1344

	TTT TCT TGG ACG CAT CGT AGT GCA ACT CTT ACA AAT ACA ATT GAT CCA Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro	450	455	460	1392
5	GAG AGA ATT AAT CAA ATA CCT TTA GTG AAA GGA TTT AGA GTT TGG GGG Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly	465	470	475	1440
10	GGC ACC TCT GTC ATT ACA GGA CCA GGA TTT ACA GGA GGG GAT ATC CTT Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu	485	490	495	1488
15	CGA AGA AAT ACC TTT GGT GAT TTT GTA TCT CTA CAA GTC AAT ATT AAT Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn	500	505	510	1536
20	TCA CCA ATT ACC CAA AGA TAC CGT TTA AGA TTT CGT TAC GCT TCC AGT Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser	515	520	525	1584
25	AGG GAT GCA CGA GTT ATA GTA TTA ACA GGA GCG GCA TCC ACA GGA GTG Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val	530	535	540	1632
30	GGA GGC CAA GTT AGT GTA AAT ATG CCT CTT CAG AAA ACT ATG GAA ATA Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile	545	550	555	1680
35	GGG GAG AAC TTA ACA TCT AGA ACA TTT AGA TAT ACC GAT TTT AGT AAT Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn	565	570	575	1728
40	CCT TTT TCA TTT AGA GCT AAT CCA GAT ATA ATT GGG ATA AGT GAA CAA Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln	580	585	590	1776
45	CCT CTA TTT GGT GCA GGT TCT ATT AGT AGC GGT GAA CTT TAT ATA GAT Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp	595	600	605	1824
50	AAA ATT GAA ATT ATT CTA GCA GAT GCA ACA TTT GAA GCA GAA TCT GAT Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp	610	615	620	1872
	TTA GAA AGA GCA CAA AAG GCG GTG AAT GCC CTG TTT ACT TCT TCC AAT Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn	625	630	635	1920
	CAA ATC GGG TTA AAA ACC GAT GTG ACG GAT TAT CAT ATT GAT CAA GTA Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val	645	650	655	1968

	TCC AAT TTA GTG GAT TGT TTA TCA GAT GAA TTT TGT CTG GAT GAA AAG Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys	660	665	670	2016
5	CGA GAA TTG TCC GAG AAA GTC AAA CAT GCG AAG CGA CTC AGT GAT GAG Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu	675	680	685	2064
10	CGG AAT TTA CTT CAA GAT CCA AAC TTC AGA GGG ATC AAT AGA CAA CCA Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro	690	695	700	2112
15	GAC CGT GGC TGG AGA GGA AGT ACA GAT ATT ACC ATC CAA GGA GGA GAT Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp	705	710	715	2160
20	GAC GTA TTC AAA GAG AAT TAC GTC ACA CTA CCG GGT ACC GTT GAT GAG Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu	725	730	735	2208
25	TGC TAT CCA ACG TAT TTA TAT CAG AAA ATA GAT GAG TCG AAA TTA AAA Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys	740	745	750	2256
30	GCT TAT ACC CGT TAT GAA TTA AGA GGG TAT ATC GAA GAT AGT CAA GAC Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp	755	760	765	2304
35	TTA GAA ATC TAT TTG ATC CGT TAC AAT GCA AAA CAC GAA ATA GTA AAT Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn	770	775	780	2352
40	GTG CCA GGC ACG GGT TCC TTA TGG CCG CTT TCA GCC CAA AGT CCA ATC Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile	785	790	795	2400
45	GGA AAG TGT GGA GAA CCG AAT CGA TGC GCG CCA CAC CTT GAA TGG AAT Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn	805	810	815	2448
50	CCT GAT CTA GAT TGT TCC TGC AGA GAC GGG GAA AAA TGT GCA CAT CAT Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His	820	825	830	2496
55	TCC CAT CAT TTC ACC TTG GAT ATT GAT GTT GGA TGT ACA GAC TTA AAT Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn	835	840	845	2544
60	GAG GAC TTA GGT GTA TGG GTG ATA TTC AAG ATT AAG ACG CAA GAT GGC Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly	850	855	860	2592

	CAT GCA AGA CTA GGG AAT CTA GAG TTT CTC GAA GAG AAA CCA TTA TTA His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu 865 870 875 880	2640
5	GGG GAA GCA CTA GCT CGT GTG AAA AGA GCG GAG AAG AAG TGG AGA GAC Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp 885 890 895	2688
10	AAA CGA GAG AAA CTG CAG TTG GAA ACA AAT ATT GTT TAT AAA GAG GCA Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala 900 905 910	2736
15	AAA GAA TCT GTA GAT GCT TTA TTT GTA AAC TCT CAA TAT GAT AGA TTA Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu 915 920 925	2784
20	CAA GTG GAT ACG AAC ATC GCA ATG ATT CAT GCG GCA GAT AAA CGC GTT Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val 930 935 940	2832
25	CAT AGA ATC CGG GAA GCG TAT CTG CCA GAG TTG TCT GTG ATT CCA GGT His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly 945 950 955 960	2880
30	GTC AAT GCG GCC ATT TTC GAA GAA TTA GAG GGA CGT ATT TTT ACA GCG Val Asn Ala Ala Ile Phe Glu Leu Glu Gly Arg Ile Phe Thr Ala 965 970 975	2928
35	TAT TCC TTA TAT GAT GCG AGA AAT GTC ATT AAA AAT GGC GAT TTC AAT Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn 980 985 990	2976
40	AAT GGC TTA TTA TGC TGG AAC GTG AAA GGT CAT GTA GAT GTA GAA GAG Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu 995 1000 1005	3024
45	CAA AAC AAC CAC CGT TCG GTC CTT GTT ATC CCA GAA TGG GAG GCA GAA Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu 1010 1015 1020	3072
50	GTG TCA CAA GAG GTT CGT GTC TGT CCA GGT CGT GGC TAT ATC CTT CGT Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg 1025 1030 1035 1040	3120
55	GTC ACA GCA TAT AAA GAG GGA TAT GGA GAG GGC TGC GTA ACG ATC CAT Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His 1045 1050 1055	3168
60	GAG ATC GAA GAC AAT ACA GAC GAA CTG AAA TTC AGC AAC TGT GTA GAA Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu 1060 1065 1070	3216

	GAG GAA GTA TAT CCA AAC AAC ACA GTA ACG TGT AAT AAT TAT ACT GGG Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly 1075 1080 1085	3264
5	ACT CAA GAA GAA TAT GAG GGT ACG TAC ACT TCT CGT AAT CAA GGA TAT Thr Gln Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr 1090 1095 1100	3312
10	GAC GAA GCC TAT GGT AAT AAC CCT TCC GTA CCA GCT GAT TAC GCT TCA Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser 1105 1110 1115 1120	3360
15	GTC TAT GAA GAA AAA TCG TAT ACA GAT GGA CGA AGA GAG AAT CCT TGT Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys 1125 1130 1135	3408
20	GAA TCT AAC AGA GGC TAT GGG GAT TAC ACA CCA CTA CCG GCT GGT TAT Glu Ser Asn Arg Gly Tyr Asp Tyr Thr Pro Leu Pro Ala Gly Tyr 1140 1145 1150	3456
25	GTA ACA AAG GAT TTA GAG TAC TTC CCA GAG ACC GAT AAG GTA TGG ATT Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile 1155 1160 1165	3504
30	GAG ATC GGA GAA ACA GAA GGA ACA TTC ATC GTG GAT AGC GTG GAA TTA Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu 1170 1175 1180	3552
35	CTC CTT ATG GAG GAA Leu Leu Met Glu Glu 1185	3567
40	(2) INFORMATION FOR SEQ ID NO:10: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1189 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10: 45 Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser 1 5 10 15 Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn 20 25 30 50 Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn 35 40 45	

	Phe	Val	Pro	Gly	Gly	Gly	Phe	Leu	Val	Gly	Leu	Ile	Asp	Phe	Val	Trp
	50						55						60			
5	Gly	Ile	Val	Gly	Pro	Ser	Gln	Trp	Asp	Ala	Phe	Leu	Val	Gln	Ile	Glu
	65				70				75					80		
	Gln	Leu	Ile	Asn	Glu	Arg	Ile	Ala	Glu	Phe	Ala	Arg	Asn	Ala	Ala	Ile
				85					90					95		
10	Ala	Asn	Leu	Glu	Gly	Leu	Gly	Asn	Asn	Phe	Asn	Ile	Tyr	Val	Glu	Ala
			100					105					110			
	Phe	Lys	Glu	Trp	Glu	Val	Asp	Pro	Asn	Asn	Pro	Gly	Thr	Arg	Thr	Arg
		115					120					125				
15	Val	Ile	Asp	Arg	Phe	Arg	Ile	Leu	Asp	Gly	Leu	Leu	Glu	Arg	Asp	Ile
		130					135				140					
20	Pro	Ser	Phe	Arg	Ile	Ser	Gly	Phe	Glu	Val	Pro	Leu	Leu	Ser	Val	Tyr
	145					150			155				160			
25	Ala	Gln	Ala	Ala	Asn	Leu	His	Leu	Ala	Ile	Leu	Arg	Asp	Ser	Val	Ile
				165					170			175				
30	Phe	Gly	Glu	Arg	Trp	Gly	Leu	Thr	Thr	Ile	Asn	Val	Asn	Glu	Asn	Tyr
			180				185				190					
35	Asn	Arg	Leu	Ile	Arg	His	Ile	Asp	Glu	Tyr	Ala	Asp	His	Cys	Ala	Asn
		195					200				205					
40	Thr	Tyr	Asn	Arg	Gly	Leu	Asn	Asn	Leu	Pro	Lys	Ser	Thr	Tyr	Gln	Asp
		210				215				220						
45	Trp	Ile	Thr	Tyr	Asn	Arg	Leu	Arg	Arg	Asp	Leu	Thr	Leu	Thr	Val	Leu
		225				230			235			240				
50	Asp	Ile	Ala	Ala	Phe	Phe	Pro	Asn	Tyr	Asp	Asn	Arg	Arg	Tyr	Pro	Ile
			245				250			255						
55	Gln	Pro	Val	Gly	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Ile
			260				265			270						
60	Asn	Phe	Asn	Pro	Gln	Leu	Gln	Ser	Val	Ala	Gln	Leu	Pro	Thr	Phe	Asn
			275				280			285						
65	Val	Met	Glu	Ser	Ser	Ala	Ile	Arg	Asn	Pro	His	Leu	Phe	Asp	Ile	Leu
			290				295			300						
70	Asn	Asn	Leu	Thr	Ile	Phe	Thr	Asp	Trp	Phe	Ser	Val	Gly	Arg	Asn	Phe
		305				310				315			320			
75	Tyr	Trp	Gly	Gly	His	Arg	Val	Ile	Ser	Ser	Leu	Ile	Gly	Gly	Asn	
			325					330			335					

Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg
 340 345 350
 Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr
 5 355 360 365
 Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg
 370 375 380
 10 Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr
 385 390 395 400
 Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp
 405 410 415
 15 Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala
 420 425 430
 Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val
 20 435 440 445
 Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro
 450 455 460
 25 Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly
 465 470 475 480
 Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu
 30 485 490 495
 Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn
 500 505 510
 Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser
 35 515 520 525
 Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val
 530 535 540
 40 Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile
 545 550 555 560
 Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn
 45 565 570 575
 Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln
 580 585 590
 50 Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp
 595 600 605
 Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp
 610 615 620

Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn
 625 630 635 640
 Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val
 5 645 650 655
 Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys
 660 665 670
 10 Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu
 675 680 685
 Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro
 15 690 695 700
 Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp
 705 710 715 720
 20 Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu
 725 730 735
 Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys
 25 740 745 750
 Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp
 30 755 760 765
 Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn
 35 770 775 780
 Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile
 40 785 790 795 800
 Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn
 45 805 810 815
 Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His
 50 820 825 830
 Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn
 835 840 845
 Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly
 45 850 855 860
 His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu
 865 870 875 880
 Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp
 50 885 890 895
 Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala
 900 905 910

	Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu			
	915	920	925	
5	Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val			
	930	935	940	
	His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly			
	945	950	955	960
10	Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala			
	965	970	975	
	Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn			
	980	985	990	
15	Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu			
	995	1000	1005	
20	Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu			
	1010	1015	1020	
25	Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg			
	1025	1030	1035	1040
30	Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His			
	1045	1050	1055	
35	Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu			
	1060	1065	1070	
40	Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly			
	1075	1080	1085	
45	Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr			
	1090	1095	1100	
50	Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser			
	1105	1110	1115	1120
55	Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys			
	1125	1130	1135	
60	Glu Ser Asn Arg Gly Tyr Asp Tyr Thr Pro Leu Pro Ala Gly Tyr			
	1140	1145	1150	
65	Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile			
	1155	1160	1165	
70	Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu			
	1170	1175	1180	
75	Leu Leu Met Glu Glu			
	1185			

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 3567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3567

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

15	ATG GAG GAA AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser 1 5 10 15	48
20	AAT CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA ACT GGT AAT Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn 20 25 30	96
25	TCA TCA ATT GAT ATT TCT CTG TCA CTT GTT CAG TTT CTG GTA TCT AAC Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn 35 40 45	144
30	TTT GTA CCA GGG GGA GGA TTT TTA GTT GGA TTA ATA GAT TTT GTA TGG Phe Val Pro Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp 50 55 60	192
35	GGA ATA GTT GGC CCT TCT CAA TGG GAT GCA TTT CTA GTA CAA ATT GAA Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu 65 70 75 80	240
40	CAA TTA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT GCT ATT Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile 85 90 95	288
45	GCT AAT TTA GAA GGA TTA GGA AAC AAT TTC AAT ATA TAT GTG GAA GCA Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala 100 105 110	336
50	TTT AAA GAA TGG GAA GAA GAT CCC CAT AAT CCA GCA ACC AGG ACC AGA Phe Lys Glu Trp Glu Glu Asp Pro His Asn Pro Ala Thr Arg Thr Arg 115 120 125	384
	GTA ATT GAT CGC TTT CGT ATA CTT GAT GGG CTA CTT GAA AGG GAC ATT Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile 130 135 140	432
	CCT TCG TTT CGA ATT TCT GGA TTT GAA GTA CCC CTT TTA TCC GTT TAT Pro Ser Phe Arg Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr 145 150 155 160	480

	GCT CAA GCG GCC AAT CTG CAT CTA GCT ATA TTA AGA GAT TCT GTA ATT Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile 165	170	175	528
5	TTT GGA GAA AGA TGG GGA TTG ACA ACG ATA AAT GTC AAT GAA AAC TAT Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr 180	185	190	576
10	AAT AGA CTA ATT AGG CAT ATT GAT GAA TAT GCT GAT CAC TGT GCA AAT Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn 195	200	205	624
15	ACG TAT AAT CGG GGA TTA AAT AAT TTA CCG AAA TCT ACG TAT CAA GAT Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp 210	215	220	672
20	TGG ATA ACA TAT AAT CGA TTA CGG AGA GAC TTA ACA TTG ACT GTA TTA Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu 225	230	235	720
25	GAT ATC GCC GCT TTC TTT CCA AAC TAT GAC AAT AGG AGA TAT CCA ATT Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile 245	250	255	768
30	CAG CCA GTT GGT CAA CTA ACA AGG GAA GTT TAT ACG GAC CCA TTA ATT Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile 260	265	270	816
35	AAT TTT AAT CCA CAG TTA CAG TCT GTA GCT CAA TTA CCT ACT TTT AAC Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn 275	280	285	864
40	GTT ATG GAG AGC AGC GCA ATT AGA AAT CCT CAT TTA TTT GAT ATA TTG Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu 290	295	300	912
45	AAT AAT CTT ACA ATC TTT ACG GAT TGG TTT AGT GTT GGA CGC AAT TTT Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe 305	310	315	960
50	TAT TGG GGA GGA CAT CGA GTA ATA TCT AGC CTT ATA GGA GGT GGT AAC Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Gly Asn 325	330	335	1008
55	ATA ACA TCT CCT ATA TAT GGA AGA GAG GCG AAC CAG GAG CCT CCA AGA Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg 340	345	350	1056
60	TCC TTT ACT TTT AAT GGA CCG GTA TTT AGG ACT TTA TCA AAT CCT ACT Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr 355	360	365	1104

	TTA CGA TTA TTA CAG CAA CCT TGG CCA GCG CCA CCA TTT AAT TTA CGT	1152
	Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg	
	370 375 380	
5	GGT GTT GAA GGA GTA GAA TTT TCT ACA CCT ACA AAT AGC TTT ACG TAT	1200
	Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr	
	385 390 395 400	
10	CGA GGA AGA GGT ACG GTT GAT TCT TTA ACT GAA TTA CCG CCT GAG GAT	1248
	Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp	
	405 410 415	
15	AAT AGT GTG CCA CCT CGC GAA GGA TAT AGT CAT CGT TTA TGT CAT GCA	1296
	Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala	
	420 425 430	
20	ACT TTT GTT CAA AGA TCT GGA ACA CCT TTT TTA ACA ACT GGT GTA GTA	1344
	Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val	
	435 440 445	
25	TTT TCT TGG ACG CAT CGT AGT GCA ACT CTT ACA AAT ACA ATT GAT CCA	1392
	Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro	
	450 455 460	
30	GAG AGA ATT AAT CAA ATA CCT TTA GTG AAA GGA TTT AGA GTT TGG GGG	1440
	Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly	
	465 470 475 480	
35	GGC ACC TCT GTC ATT ACA GGA CCA GGA TTT ACA GGA GGG GAT ATC CTT	1488
	Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu	
	485 490 495	
40	CGA AGA AAT ACC TTT GGT GAT TTT GTA TCT CTA CAA GTC AAT ATT AAT	1536
	Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn	
	500 505 510	
45	TCA CCA ATT ACC CAA AGA TAC CGT TTA AGA TTT CGT TAC GCT TCC AGT	1584
	Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser	
	515 520 525	
50	AGG GAT GCA CGA GTT ATA GTA TTA ACA GGA GCG GCA TCC ACA GGA GTG	1632
	Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val	
	530 535 540	
55	GGA GGC CAA GTT AGT GTA AAT ATG CCT CTT CAG AAA ACT ATG GAA ATA	1680
	Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile	
	545 550 555 560	
60	GGG GAG AAC TTA ACA TCT AGA ACA TTT AGA TAT ACC GAT TTT AGT AAT	1728
	Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn	
	565 570 575	

	CCT TTT TCA TTT AGA GCT AAT CCA GAT ATA ATT GGG ATA AGT GAA CAA Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln	580	585	590	1776
5	CCT CTA TTT GGT GCA GGT TCT ATT AGT AGC GGT GAA CTT TAT ATA GAT Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp	595	600	605	1824
10	AAA ATT GAA ATT ATT CTA GCA GAT GCA ACA TTT GAA GCA GAA TCT GAT Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp	610	615	620	1872
15	TTA GAA AGA GCA CAA AAG GCG GTG AAT GCC CTG TTT ACT TCT TCC AAT Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn	625	630	635	1920
20	CAA ATC GGG TTA AAA ACC GAT GTG ACG GAT TAT CAT ATT GAT CAA GTA Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val	645	650	655	1968
25	TCC AAT TTA GTG GAT TGT TTA TCA GAT GAA TTT TGT CTG GAT GAA AAG Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys	660	665	670	2016
30	CGA GAA TTG TCC GAG AAA GTC AAA CAT GCG AAG CGA CTC AGT GAT GAG Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu	675	680	685	2064
35	CGG AAT TTA CTT CAA GAT CCA AAC TTC AGA GGG ATC AAT AGA CAA CCA Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro	690	695	700	2112
40	GAC CGT GGC TGG AGA GGA AGT ACA GAT ATT ACC ATC CAA GGA GGA GAT Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp	705	710	715	2160
45	GAC GTA TTC AAA GAG AAT TAC GTC ACA CTA CCG GGT ACC GTT GAT GAG Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu	725	730	735	2208
50	TGC TAT CCA ACG TAT TTA TAT CAG AAA ATA GAT GAG TCG AAA TTA AAA Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys	740	745	750	2256
	GCT TAT ACC CGT TAT GAA TTA AGA GGG TAT ATC GAA GAT AGT CAA GAC Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp	755	760	765	2304
	TTA GAA ATC TAT TTG ATC CGT TAC AAT GCA AAA CAC GAA ATA GTA AAT Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn	770	775	780	2352

	GTC CCA GGC ACG GGT TCC TTA TGG CCG CTT TCA GCC CAA AGT CCA ATC Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile 785	790	795	800	2400
5	GGA AAG TGT GGA GAA CCG AAT CGA TGC GCG CCA CAC CTT GAA TGG AAT Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn 805	810		815	2448
10	CCT GAT CTA GAT TGT TCC TGC AGA GAC GGG GAA AAA TGT GCA CAT CAT Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His 820	825		830	2496
15	TCC CAT CAT TTC ACC TTG GAT ATT GAT GTT GGA TGT ACA GAC TTA AAT Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn 835	840		845	2544
20	GAG GAC TTA GGT GTA TGG GTG ATA TTC AAG ATT AAG ACG CAA GAT GGC Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly 850	855		860	2592
25	CAT GCA AGA CTA GGG AAT CTA GAG TTT CTC GAA GAG AAA CCA TTA TTA His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu 865	870	875	880	2640
30	GGG GAA GCA CTA GCT CGT GTG AAA AGA GCG GAG AAG TGG AGA GAC Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp 885	890		895	2688
35	AAA CGA GAG AAA CTG CAG TTG GAA ACA AAT ATT GTT TAT AAA GAG GCA Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala 900	905		910	2736
40	AAA GAA TCT GTA GAT GCT TTA TTT GTA AAC TCT CAA TAT GAT AGA TTA Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu 915	920		925	2784
45	CAA GTG GAT ACG AAC ATC GCA ATG ATT CAT GCG GCA GAT AAA CGC GTT Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val 930	935	940		2832
50	CAT AGA ATC CGG GAA GCG TAT CTG CCA GAG TTG TCT GTG ATT CCA GGT His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly 945	950	955	960	2880
	GTC AAT GCG GCC ATT TTC GAA GAA TTA GAG GGA CGT ATT TTT ACA GCG Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala 965	970		975	2928
	TAT TCC TTA TAT GAT GCG AGA AAT GTC ATT AAA AAT GGC GAT TTC AAT Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn 980	985		990	2976

	AAT GGC TTA TTA TGC TGG AAC GTG AAA GGT CAT GTA GAT GTA GAA GAG Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu 995	1000	1005	3024
5	CAA AAC AAC CAC CGT TCG GTC CTT GTT ATC CCA GAA TGG GAG GCA GAA Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu 1010	1015	1020	3072
10	GTG TCA CAA GAG GTT CGT GTC TGT CCA GGT CGT GGC TAT ATC CTT CGT Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg 1025	1030	1035	3120
15	GTC ACA GCA TAT AAA GAG GGA TAT GGA GAG GGC TGC GTA ACG ATC CAT Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His 1045	1050	1055	3168
20	GAG ATC GAA GAC AAT ACA GAC GAA CTG AAA TTC AGC AAC TGT GTA GAA Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu 1060	1065	1070	3216
25	GAG GAA GTA TAT CCA AAC ACA GCA ACG TGT AAT AAT TAT ACT GGG Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly 1075	1080	1085	3264
30	ACT CAA GAA GAA TAT GAG GGT ACG TAC ACT TCT CGT AAT CAA GGA TAT Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr 1090	1095	1100	3312
35	GAC GAA GCC TAT GGT AAT AAC CCT TCC GTA CCA GCT GAT TAC GCT TCA Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser 1105	1110	1115	3360
40	GTC TAT GAA GAA AAA TCG TAT ACA GAT GGA CGA AGA GAG AAT CCT TGT Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys 1125	1130	1135	3408
45	GAA TCT AAC AGA GGC TAT GGG GAT TAC ACA CCA CTA CCG GCT GGT TAT Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr 1140	1145	1150	3456
50	GTA ACA AAG GAT TTA GAG TAC TTC CCA GAG ACC GAT AAG GTA TGG ATT Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile 1155	1160	1165	3504
	GAG ATC GGA GAA ACA GAA GGA ACA TTC ATC GTG GAT AGC GTG GAA TTA Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu 1170	1175	1180	3552
	CTC CTT ATG GAG GAA Leu Leu Met Glu Glu 1185			3567

(2) INFORMATION FOR SEQ ID NO:12:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1189 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

15 Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
1 5 10 15

15 Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn
20 25 30

20 Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn
35 40 45

20 Phe Val Pro Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp
50 55 60

25 Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu
65 70 75 80

30 Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile
85 90 95

35 Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala
100 105 110

40 Phe Lys Glu Trp Glu Glu Asp Pro His Asn Pro Ala Thr Arg Thr Arg
115 120 125

45 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile
130 135 140

50 Pro Ser Phe Arg Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr
145 150 155 160

50 Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile
165 170 175

55 Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr
180 185 190

60 Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn
195 200 205

65 Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp
210 215 220

70 Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu
225 230 235 240

	Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile			
	245	250	255	
5	Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile			
	260	265	270	
	Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn			
	275	280	285	
10	Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu			
	290	295	300	
	Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe			
15	305	310	315	320
	Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Gly Asn			
	325	330	335	
20	Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg			
	340	345	350	
25	Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr			
	355	360	365	
30	Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg			
	370	375	380	
35	Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr			
	385	390	395	400
40	Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp			
	405	410	415	
45	Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala			
	420	425	430	
	Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val			
	435	440	445	
	Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro			
	450	455	460	
	Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly			
	465	470	475	480
	Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu			
	485	490	495	
50	Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn			
	500	505	510	
	Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser			
	515	520	525	

	Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val			
	530	535	540	
5	Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile			
	545	550	555	560
	Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn			
	565	570	575	
10	Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln			
	580	585	590	
15	Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp			
	595	600	605	
	Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp			
	610	615	620	
20	Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn			
	625	630	635	640
	Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val			
	645	650	655	
25	Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys			
	660	665	670	
30	Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu			
	675	680	685	
35	Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro			
	690	695	700	
	Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp			
	705	710	715	720
	Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu			
	725	730	735	
40	Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys			
	740	745	750	
	Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp			
45	755	760	765	
	Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn			
	770	775	780	
50	Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile			
	785	790	795	800
	Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn			
	805	810	815	

	Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His			
	820	825	830	
5	Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn			
	835	840	845	
	Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly			
	850	855	860	
10	His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu			
	865	870	875	880
15	Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp			
	885	890	895	
	Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala			
	900	905	910	
20	Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu			
	915	920	925	
25	Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val			
	930	935	940	
30	His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly			
	945	950	955	960
35	Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala			
	965	970	975	
40	Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn			
	980	985	990	
45	Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu			
	995	1000	1005	
50	Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu			
	1010	1015	1020	
	Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg			
	1025	1030	1035	1040
	Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His			
	1045	1050	1055	
	Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu			
	1060	1065	1070	
55	Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly			
	1075	1080	1085	
	Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr			
	1090	1095	1100	

Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser
1105 1110 1115 1120

5 Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys
1125 1130 1135

Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
1140 1145 1150

10 Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile
1155 1160 1165

Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
15 1170 1175 1180

Leu Leu Met Glu Glu
1185

20 (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCATTTAAAG AATGGGAAGA AGATAATAAT CCAGCAACCA GGACCAGAG

49

30 (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCATTTAAAG AATGGGAAGA AGATCCTAAT GCAAATCCAG CAACCAGGAC CAGAG

55

45 (2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCCCGATCGGC CGCATGC

17

5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCATTTAAAG AATGGGAAGG GATCCTAGGA ATCCAGAAC CAGGACCAGA G

51

20 (2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAGCTCTTGT TAAAAAAAGGT GTTCCAGATC

30

35 (2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

45 (ix) FEATURE:

- (A) NAME/KEY: modified_base
(B) LOCATION: 19..39
(D) OTHER INFORMATION: /note= "N = G, A, T or C"

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCATTTAAAG AATGGGAANN NNNNNNNNNN NNNNNNNNNNA CCAGGACCAG AGTAATTGAT

60

50 CG

62

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Glu Asp Pro Asn Asn Pro Ala
1 5

- (2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCATTAAAG AATGGGAAGG GATCCTAGGA ATCCAGCAAC CAGGACCAGA G

51

- (2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCATTTAAAG AATGGGAAGA TGATCCTCAT AATCCCACAA CCAGGACCG AGTAATTGAT

60

CGC

63

- (2) INFORMATION FOR SEO ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Asp Asp Pro His Asn Pro Thr
1 5

5 (2) INFORMATION FOR SEQ ID NO:27:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

20 Val Asp Pro Asn Asn Pro Gly
1 5

25 (2) INFORMATION FOR SEQ ID NO:28:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

40 Thr Asn Pro Ala Leu Arg Glu Glu Met Arg Ile Gln Phe Asn Asp Met
1 5 10 15

45 Asn Ser Ala Leu Thr Thr Ala Ile Pro Leu Leu Ala Val Gln Asn Tyr
20 25 30

50 Gln Val Pro Leu Leu Ser Val Tyr Val Gln Ala Ala Asn Leu His Leu
35 40 45

55 Ser Val
50

60 (2) INFORMATION FOR SEQ ID NO:29:

65 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

75 Thr Asn Pro Ala Leu Thr Glu Glu Met Arg Ile Gln Phe Asn Asp Met
1 5 10 15

80 Asn Ser Ala Leu Thr Thr Ala Ile Pro Leu Phe Thr Val Gln Asn Tyr
20 25 30

Gln Val Pro Leu Leu Ser Val Tyr Val Gln Ala Ala Asn Leu His Leu
35 40 45

Ser Val
5 50

(2) INFORMATION FOR SEQ ID NO:30:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Thr Asn Pro Ala Leu Arg Glu Glu Met Arg Ile Gln Phe Asn Asp Met
1 5 10 15

Asn Ser Ala Leu Thr Thr Ala Ile Pro Leu Phe Ala Val Gln Asn Tyr
20 25 30

Gln Val Pro Leu Leu Ser Val Tyr Val Gln Ala Ala Asn Leu His Leu
35 40 45

Ser Val
50

20 (2) INFORMATION FOR SEQ ID NO:31:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

35 Thr Asn Pro Ala Leu Arg Glu Glu Met Arg Ile Gln Phe Asn Asp Met
1 5 10 15

40 Asn Ser Ala Leu Thr Thr Ala Ile Pro Leu Phe Thr Val Gln Asn Tyr
20 25 30

45 Gln Val Pro Leu Leu Ser Val Tyr Val Gln Ala Val Asn Leu His Leu
35 40 45

50 Ser Val
50

(2) INFORMATION FOR SEQ ID NO:32:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

10 Thr Asn Pro Ala Leu Arg Glu Glu Met Arg Ile Gln Phe Asn Asp Met
1 5 10 15

15 Asn Ser Ala Leu Thr Thr Ala Ile Pro Leu Phe Ala Val Gln Asn Tyr
20 25 30

Gln Val Pro Leu Leu Ser Val Tyr Val Gln Ala Ala Asn Leu His Leu
35 40 45

20 Ser Val
25 50

25 (2) INFORMATION FOR SEQ ID NO:33:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Asn Asn Ala Gln Leu Arg Glu Asp Val Arg Ile Arg Phe Ala Asn Thr
1 5 10 15

40 Asp Asp Ala Leu Ile Thr Ala Ile Asn Asn Phe Thr Leu Thr Ser Phe
20 25 30

Glu Ile Pro Leu Leu Ser Val Tyr Val Gln Ala Ala Asn Leu His Leu
35 40 45

45 Ser Leu
50 50

(2) INFORMATION FOR SEQ ID NO:34:

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Asn Asn Ala Gln Leu Arg Glu Asp Val Arg Ile Arg Phe Ala Asn Thr
1 5 10 15

5 Asp Asp Ala Leu Ile Thr Ala Ile Asn Asn Phe Thr Leu Thr Ser Phe
20 25 30

Glu Ile Pro Leu Leu Ser Val Tyr Val Gln Ala Ala Asn Leu His Leu
10 35 40 45

Ser Leu
50

15 (2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Asn Asn Pro Ala Ser Gln Glu Arg Val Arg Thr Arg Phe Arg Leu Thr
20 1 5 10 15

Asp Asp Ala Ile Val Thr Gly Leu Pro Thr Leu Ala Ile Arg Asn Leu
30 20 25 30

Glu Val Val Asn Leu Ser Val Tyr Thr Gln Ala Ala Asn Leu His Leu
35 30 35 40 45

Ser Leu
50

(2) INFORMATION FOR SEQ ID NO:36:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Asn Asn Pro Glu Thr Arg Thr Arg Val Ile Asp Arg Phe Arg Ile Leu
50 1 5 10 15

Asp Gly Leu Leu Glu Arg Asp Ile Pro Ser Phe Arg Ile Ser Gly Phe
20 25 30

Glu Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Ala Asn Leu His Leu
35 40 45

Ala Ile
5 50

(2) INFORMATION FOR SEQ ID NO:37:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Asp Asn Pro Val Thr Arg Thr Arg Val Val Asp Arg Phe Arg Ile Leu
1 5 10 15

Asp Gly Leu Leu Glu Arg Asp Ile Pro Ser Phe Arg Ile Ala Gly Phe
20 25 30

Glu Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Ala Asn Leu His Leu
35 40 45

Ala Ile
50

20 (2) INFORMATION FOR SEQ ID NO:38:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

35 Thr Asn Pro Ala Leu Lys Glu Glu Met Arg Thr Gln Phe Asn Asp Met
1 5 10 15

40 Asn Ser Ile Leu Val Thr Ala Ile Pro Leu Phe Ser Val Gln Asn Tyr
20 25 30

45 Gln Val Pro Phe Leu Ser Val Tyr Val Gln Ala Ala Asn Leu His Leu
35 40 45

50 Ser Val
50

(2) INFORMATION FOR SEQ ID NO:39:

Glu Ile Pro Leu Leu Thr Val Tyr Val Gln Ala Ala Asn Leu His Leu
35 40 45

Ser Leu
5 50

(2) INFORMATION FOR SEQ ID NO:44:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Asp Asn Glu Ala Ala Lys Ser Arg Val Ile Asp Arg Phe Arg Ile Leu
1 5 10 15

Asp Gly Leu Ile Glu Ala Asn Ile Pro Ser Phe Arg Ile Ile Gly Phe
20 25 30

Glu Val Pro Leu Leu Ser Val Tyr Val Gln Ala Ala Asn Leu His Leu
35 40 45

Ala Leu
50

20 (2) INFORMATION FOR SEQ ID NO:45:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

40 Asp Asn Thr Ala Ala Arg Ser Arg Val Thr Glu Arg Phe Arg Ile Ile
1 5 10 15

45 Asp Ala Gln Ile Glu Ala Asn Ile Pro Ser Phe Arg Ile Pro Gly Phe
20 25 30

Glu Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Ala Asn Leu His Leu
35 40 45

50 Ala Leu
50

(2) INFORMATION FOR SEQ ID NO:46:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Asp Asp Ala Arg Thr Arg Ser Val Leu Tyr Thr Gln Tyr Ile Ala Leu
1 5 10 15

Glu Leu Asp Phe Leu Asn Ala Met Pro Leu Phe Ala Ile Arg Asn Gln
20 25 30

Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu His Leu
35 40 45

Leu Leu
50

20 (2) INFORMATION FOR SEQ ID NO:47:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Asn Asp Ala Arg Ser Arg Ser Ile Ile Leu Glu Arg Tyr Val Ala Leu
1 5 10 15

Glu Leu Asp Ile Thr Thr Ala Ile Pro Leu Phe Arg Ile Arg Asn Glu
20 25 30

Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu His Leu
35 40 45

Leu Leu
50

45

(2) INFORMATION FOR SEQ ID NO:48:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Asn Asp Ala Arg Ser Arg Ser Ile Ile Leu Glu Arg Tyr Val Ala Leu
1 5 10 15

5 Glu Leu Asp Ile Thr Thr Ala Ile Pro Leu Phe Arg Ile Arg Asn Glu
20 25 30

Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu His Leu
35 40 45

10 Leu Leu
50

15 (2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Asn Asp Ala Arg Ser Arg Ser Ile Ile Arg Glu Arg Tyr Ile Ala Leu
1 5 10 15

Glu Leu Asp Ile Thr Thr Ala Ile Pro Leu Phe Ser Ile Arg Asn Glu
20 25 30

Glu Val Pro Leu Leu Met Val Tyr Ala Gln Ala Ala Asn Leu His Leu
35 40 45

Leu Leu
50

(2) INFORMATION FOR SEQ ID NO:50:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Asn Asn Thr Arg Ala Arg Ser Val Val Lys Ser Gln Tyr Ile Ala Leu
1 5 10 15

Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe Ala Val Ser Gly Glu
20 25 30

Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala Ala Asn Leu His Leu
35 40 45

5 Leu Leu
50

(2) INFORMATION FOR SEQ ID NO:51:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Asn Asn Thr Arg Ala Arg Ser Val Val Lys Asn Gln Tyr Ile Ala Leu
1 5 10 15

20 Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe Ala Val Ser Gly Glu
20 25 30

Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala Ala Asn Leu His Leu
35 40 45

Leu Leu
50

30 (2) INFORMATION FOR SEQ ID NO:52:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

45 GGATCCCTCG AGCTGCAGGA GC 22

45 (2) INFORMATION FOR SEQ ID NO:53:

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ix) FEATURE:
(A) NAME/KEY: modified_base
(B) LOCATION: 31..33

(D) OTHER INFORMATION: /note= "N = C, A, T or G"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

5 GGGCTACTTG AAAGGGACAT TCCTTCGTTT NNNATTCTG GATTTGAAGT ACCCC 55

(2) INFORMATION FOR SEQ ID NO:54:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15 (xii) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GCATTTAAAG AATGGGAAGT AGATCCTAAT AACCTGGAA CCAGGACCAG AGTAATTGAT 60

20 CGC 63

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Val Asp Pro Asn Asn Pro Gly
1 5

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

45 (xii) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GCATTTAAAG AATGGGAAGA AGATCCCCAT AACCCAGCAA CCAGGACCAG AGTAATTGAT 60

CGC 63

50

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Glu Asp Pro His Asn Pro Ala
 1 5

10

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 3567 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..3567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ATG GAG GAA AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT
 Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
 1 5 10 15

48

AAT CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA ACT GGT AAT
 Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn
 20 25 30

96

TCA TCA ATT GAT ATT TCT CTG TCA CTT GTT CAG TTT CTG GTA TCT AAC
 Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn
 35 40 45

144

TTT GTA CCA GGG GGA TTT TTA GTT GGA TTA ATA GAT TTT GTA TGG
 Phe Val Pro Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp
 50 55 60

192

GGA ATA GTT GGC CCT TCT CAA TGG GAT GCA TTT CTA GTA CAA ATT GAA
 Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu
 65 70 75 80

240

CAA TTA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT GCT ATT
 Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile
 85 90 95

288

45

50 GCT AAT TTA GAA GGA TTA GGA AAC AAT TTC AAT ATA TAT GTG GAA GCA
 Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala
 100 105 110

336

	TTT AAA GAA TGG GAA GAA GAT CCT AAT AAT CCA GCA ACC AGG ACC AGA Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg	115 120 125	384
5	GTA ATT GAT CGC TTT CGT ATA CTT GAT GGG CTA CTT GAA AGG GAC ATT Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile	130 135 140	432
10	CCT TCG TTT GCA ATT TCT GGA TTT GAA GTA CCC CTT TTA TCC GTT TAT Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr	145 150 155	480
15	GCT CAA GCG GCC AAT CTG CAT CTA GCT ATA TTA AGA GAT TCT GTA ATT Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile	165 170 175	528
20	TTT GGA GAA AGA TGG GGA TTG ACA ACG ATA AAT GTC AAT GAA AAC TAT Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr	180 185 190	576
25	AAT AGA CTA ATT AGG CAT ATT GAT GAA TAT GCT GAT CAC TGT GCA AAT Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn	195 200 205	624
30	ACG TAT AAT CGG GGA TTA AAT AAT TTA CCG GCT AGC ACG TAT CAA GAT Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Ala Ser Thr Tyr Gln Asp	210 215 220	672
35	TGG ATA ACA TAT AAT CGA TTA CGG AGA GAC TTA ACA TTG ACT GTA TTA Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu	225 230 235	720
40	GAT ATC GCC GCT TTC TTT CCA AAC TAT GAC AAT AGG AGA TAT CCA ATT Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile	245 250 255	768
45	CAG CCA GTT GGT CAA CTA ACA AGG GAA GTT TAT ACG GAC CCA TTA ATT Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile	260 265 270	816
50	AAT TTT AAT CCA CAG TTA CAG TCT GTA GCT CAA TTA CCT ACT TTT AAC Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn	275 280 285	864
	GTT ATG GAG AGC AGC GCA ATT AGA AAT CCT CAT TTA TTT GAT ATA TTG Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu	290 295 300	912
	AAT AAT CTT ACA ATC TTT ACG GAT TGG TTT AGT GTT GGA CGC AAT TTT Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe	305 310 315	960

	TAT TGG GGA GGA CAT CGA GTA ATA TCT AGC CTT ATA GGA GGT GGT AAC Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Asn 325	330	335	1008	
5	ATA ACA TCT CCT ATA TAT GGA AGA GAG GCG AAC CAG GAG CCT CCA AGA Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg 340	345	350	1056	
10	TCC TTT ACT TTT AAT GGA CCG GTA TTT AGG ACT TTA TCA AAT CCT ACT Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr 355	360	365	1104	
15	TTA CGA TTA TTA CAG CAA CCT TGG CCA GCG CCA CCA TTT AAT TTA CGT Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg 370	375	380	1152	
20	GGT GTT GAA GGA GTA GAA TTT TCT ACA CCT ACA AAT AGC TTT ACG TAT Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr 385	390	395	1200	
25	CGA GGA AGA GGT ACG GTT GAT TCT TTA ACT GAA TTA CCG CCT GAG GAT Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp 405	410	415	1248	
30	AAT AGT GTG CCA CCT CGC GAA GGA TAT AGT CAT CGT TTA TGT CAT GCA Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala 420	425	430	1296	
35	ACT TTT GTT CAA AGA TCT GGA ACA CCT TTT TTA ACA ACT GGT GTA GTA Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val 435	440	445	1344	
40	TTT TCT TGG ACG CAT CGT AGT GCA ACT CTT ACA AAT ACA ATT GAT CCA Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro 450	455	460	1392	
45	GAG AGA ATT AAT CAA ATA CCT TTA GTG AAA GGA TTT AGA GTT TGG GGG Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly 465	470	475	1440	
50	480	485	490	495	1488
55	CGA AGA AAT ACC TTT GGT GAT TTT GTA TCT CTA CAA GTC AAT ATT AAT Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn 500	505	510	1536	
60	TCA CCA ATT ACC CAA AGA TAC CGT TTA AGA TTT CGT TAC GCT TCC AGT Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser 515	520	525	1584	

	AGG GAT GCA CGA GTT ATA GTA TTA ACA GGA GCG GCA TCC ACA GGA GTG		1632
	Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val		
	530	535	540
5	GGA GGC CAA GTT AGT GTA AAT ATG CCT CTT CAG AAA ACT ATG GAA ATA		1680
	Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile		
	545	550	560
10	GGG GAG AAC TTA ACA TCT AGA ACA TTT AGA TAT ACC GAT TTT AGT AAT		1728
	Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn		
	565	570	575
15	CCT TTT TCA TTT AGA GCT AAT CCA GAT ATA ATT GGG ATA AGT GAA CAA		1776
	Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln		
	580	585	590
20	CCT CTA TTT GGT GCA GGT TCT ATT AGT AGC GGT GAA CTT TAT ATA GAT		1824
	Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp		
	595	600	605
25	AAA ATT GAA ATT ATT CTA GCA GAT GCA ACA TTT GAA GCA GAA TCT GAT		1872
	Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp		
	610	615	620
30	TTA GAA AGA GCA CAA AAG GCG GTG AAT GCC CTG TTT ACT TCT TCC AAT		1920
	Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn		
	625	630	635
	640		
35	CAA ATC GGG TTA AAA ACC GAT GTG ACG GAT TAT CAT ATT GAT CAA GTA		1968
	Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val		
	645	650	655
40	TCC AAT TTA GTG GAT TGT TTA TCA GAT GAA TTT TGT CTG GAT GAA AAG		2016
	Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys		
	660	665	670
45	CGA GAA TTG TCC GAG AAA GTC AAA CAT GCG AAG CGA CTC AGT GAT GAG		2064
	Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu		
	675	680	685
50	CGG AAT TTA CTT CAA GAT CCA AAC TTC AGA GGG ATC AAT AGA CAA CCA		2112
	Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro		
	690	695	700
55	GAC CGT GGC TGG AGA GGA AGT ACA GAT ATT ACC ATC CAA GGA GGA GAT		2160
	Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp		
	705	710	715
60	GAC GTA TTC AAA GAG AAT TAC GTC ACA CTA CCG GGT ACC GTT GAT GAG		2208
	Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu		
	725	730	735

	TGC TAT CCA ACG TAT TTA TAT CAG AAA ATA GAT GAG TCG AAA TTA AAA Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys	740	745	750	2256
5	GCT TAT ACC CGT TAT GAA TTA AGA GGG TAT ATC GAA GAT AGT CAA GAC Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp	755	760	765	2304
10	TTA GAA ATC TAT TTG ATC CGT TAC AAT GCA AAA CAC GAA ATA GTA AAT Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn	770	775	780	2352
15	GTG CCA GGC ACG GGT TCC TTA TGG CCG CTT TCA GCC CAA AGT CCA ATC Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile	785	790	795	2400
20	GGA AAG TGT GGA GAA CCG AAT CGA TGC GCG CCA CAC CTT GAA TGG AAT Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn	805	810	815	2448
25	CCT GAT CTA GAT TGT TCC TGC AGA GAC GGG GAA AAA TGT GCA CAT CAT Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His	820	825	830	2496
30	TCC CAT CAT TTC ACC TTG GAT ATT GAT GTT GGA TGT ACA GAC TTA AAT Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn	835	840	845	2544
35	GAG GAC TTA GGT GTA TGG GTG ATA TTC AAG ATT AAG ACG CAA GAT GGC Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly	850	855	860	2592
40	CAT GCA AGA CTA GGG AAT CTA GAG TTT CTC GAA GAG AAA CCA TTA TTA His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu	865	870	875	2640
45	GGG GAA GCA CTA GCT CGT GTG AAA AGA GCG GAG AAG AAG TGG AGA GAC Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp	885	890	895	2688
50	AAA CGA GAG AAA CTG CAG TTG GAA ACA AAT ATT GTT TAT AAA GAG GCA Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala	900	905	910	2736
55	AAA GAA TCT GTA GAT GCT TTA TTT GTA AAC TCT CAA TAT GAT AGA TTA Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu	915	920	925	2784
60	CAA GTG GAT ACG AAC ATC GCA ATG ATT CAT GCG GCA GAT AAA CGC GTT Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val	930	935	940	2832

	CAT AGA ATC CGG GAA GCG TAT CTG CCA GAG TTG TCT GTG ATT CCA GGT		2880
	His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly		
945	950	955	960
5	GTC AAT GCG GCC ATT TTC GAA GAA TTA GAG GGA CGT ATT TTT ACA GCG		2928
	Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala		
	965	970	975
10	TAT TCC TTA TAT GAT GCG AGA AAT GTC ATT AAA AAT GGC GAT TTC AAT		2976
	Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn		
	980	985	990
15	AAT GGC TTA TTA TGC TGG AAC GTG AAA GGT CAT GTA GAT GTA GAA GAG		3024
	Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu		
	995	1000	1005
20	CAA AAC AAC CAC CGT TCG GTC CTT GTT ATC CCA GAA TGG GAG GCA GAA		3072
	Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu		
	1010	1015	1020
25	GTG TCA CAA GAG GTT CGT GTC TGT CCA GGT CGT GGC TAT ATC CTT CGT		3120
	Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg		
	1025	1030	1035
30	GTC ACA GCA TAT AAA GAG GGA TAT GGA GAG GGC TGC GTA ACG ATC CAT		3168
	Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His		
	1045	1050	1055
35	GAG ATC GAA GAC AAT ACA GAC GAA CTG AAA TTC AGC AAC TGT GTA GAA		3216
	Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu		
	1060	1065	1070
40	GAG GAA GTA TAT CCA AAC AAC ACA GTA ACG TGT AAT AAT TAT ACT GGG		3264
	Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly		
	1075	1080	1085
45	ACT CAA GAA GAA TAT GAG GGT ACG TAC ACT TCT CGT AAT CAA GGA TAT		3312
	Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr		
	1090	1095	1100
50	GAC GAA GCC TAT GGT AAT AAC CCT TCC GTA CCA GCT GAT TAC GCT TCA		3360
	Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser		
	1105	1110	1115
			1120
55	GTC TAT GAA GAA AAA TCG TAT ACA GAT GGA CGA AGA GAG AAT CCT TGT		3408
	Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys		
	1125	1130	1135
60	GAA TCT AAC AGA GGC TAT GGG GAT TAC ACA CCA CTA CCG GCT GGT TAT		3456
	Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr		
	1140	1145	1150

	GTA ACA AAG GAT TTA GAG TAC TTC CCA GAG ACC GAT AAG GTA TGG ATT	3504
	Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile	
	1155 1160 1165	
5	GAG ATC GGA GAA ACA GAA GGA ACA TTC ATC GTG GAT AGC GTG GAA TTA	3552
	Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu	
	1170 1175 1180	
10	CTC CTT ATG GAG GAA	3567
	Leu Leu Met Glu Glu	
	1185	

(2) INFORMATION FOR SEQ ID NO:59:

15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1189 amino acids	
	(B) TYPE: amino acid	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: protein	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:	
25	Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser	
	1 5 10 15	
30	Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn	
	20 25 30	
35	Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn	
	35 40 45	
40	Phe Val Pro Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp	
	50 55 60	
45	Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu	
	65 70 75 80	
50	Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile	
	85 90 95	
	Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala	
	100 105 110	
55	Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg	
	115 120 125	
60	Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile	
	130 135 140	
65	Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr	
	145 150 155 160	

	Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile		
	165	170	175
	Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr		
5	180	185	190
	Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn		
	195	200	205
10	Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Ala Ser Thr Tyr Gln Asp		
	210	215	220
	Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu		
	225	230	235
15	240		
	Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile		
	245	250	255
20	Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile		
	260	265	270
25	Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn		
	275	280	285
30	Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu		
	290	295	300
35	Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe		
	305	310	315
40	320		
	Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Asn		
	325	330	335
	Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg		
	340	345	350
45	Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr		
	355	360	365
50	Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg		
	370	375	380
	Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr		
	385	390	395
55	400		
	Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp		
	405	410	415
	Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala		
	420	425	430
60	Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val		
	435	440	445

	Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro		
	450	455	460
	Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly		
5	465	470	475
	Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu		
	485	490	495
10	Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn		
	500	505	510
	Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser		
15	515	520	525
	Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val		
	530	535	540
20	Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile		
	545	550	555
	560		
	Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn		
	565	570	575
25	Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln		
	580	585	590
	595		
30	Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp		
	595	600	605
	Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp		
	610	615	620
35	625		
	Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn		
	630	635	640
	645		
40	Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val		
	645	650	655
	660		
	Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys		
	660	665	670
	675		
45	Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu		
	680	685	
	690		
	Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro		
	695	700	
50	Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp		
	705	710	715
	725		
	Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu		
	730	735	

	Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys		
	740	745	750
5	Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp		
	755	760	765
	Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn		
	770	775	780
10	Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile		
	785	790	795
	Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn		
	805	810	815
15	Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His		
	820	825	830
20	Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn		
	835	840	845
25	Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly		
	850	855	860
30	His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu		
	865	870	875
35	Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp		
	885	890	895
40	Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala		
	900	905	910
45	Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu		
	915	920	925
50	Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val		
	930	935	940
	His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly		
	945	950	955
	Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala		
	965	970	975
	Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn		
	980	985	990
	Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu		
	995	1000	1005
	Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu		
	1010	1015	1020

Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg
 1025 1030 1035 1040
 Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His
 5 1045 1050 1055
 Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu
 1060 1065 1070
 10 Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly
 1075 1080 1085
 Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr
 1090 1095 1100
 15 Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser
 1105 1110 1115 1120
 Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys
 20 1125 1130 1135
 Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
 1140 1145 1150
 Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile
 25 1155 1160 1165
 Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
 1170 1175 1180
 30 Leu Leu Met Glu Glu
 1185
 35 (2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3567 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: CDS
 45 (B) LOCATION: 1..3567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATG GAG GAA AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT
 50 Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
 1 5 10 15

48

	AAT CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA ACT GGT AAT		96
	Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn		
	20 25 30		
5	TCA TCA ATT GAT ATT TCT CTG TCA CTT GTT CAG TTT CTG GTA TCT AAC		144
	Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn		
	35 40 45		
10	TTT GTA CCA GGG GGA GGA TTT TTA GTT GGA TTA ATA GAT TTT GTA TGG		192
	Phe Val Pro Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp		
	50 55 60		
15	GGA ATA GTT GGC CCT TCT CAA TGG GAT GCA TTT CTA GTA CAA ATT GAA		240
	Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu		
	65 70 75 80		
20	CAA TTA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT GCT ATT		288
	Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile		
	85 90 95		
25	GCT AAT TTA GAA GGA TTA GGA AAC AAT TTC AAT ATA TAT GTG GAA GCA		336
	Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala		
	100 105 110		
30	TTT AAA GAA TGG GAA GAA GAT CCT AAT AAT CCA GCA ACC AGG ACC AGA		384
	Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg		
	115 120 125		
35	GTA ATT GAT CGC TTT CGT ATA CTT GAT GGG CTA CTT GAA AGG GAC ATT		432
	Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile		
	130 135 140		
40	CCT TCG TTT GAC ATT TCT GGA TTT GAA GTA CCC CTT TTA TCC GTT TAT		480
	Pro Ser Phe Asp Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr		
	145 150 155 160		
45	GCT CAA GCG GCC AAT CTG CAT CTA GCT ATA TTA AGA GAT TCT GTA ATT		528
	Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile		
	165 170 175		
50	TTT GGA GAA AGA TGG GGA TTG ACA ACG ATA AAT GTC AAT GAA AAC TAT		576
	Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr		
	180 185 190		
55	AAT AGA CTA ATT AGG CAT ATT GAT GAA TAT GCT GAT CAC TGT GCA AAT		624
	Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn		
	195 200 205		
60	ACG TAT AAT CGG GGA TTA AAT AAT TTA CCG GCT AGC ACG TAT CAA GAT		672
	Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Ala Ser Thr Tyr Gln Asp		
	210 215 220		

	TGG ATA ACA TAT AAT CGA TTA CGG AGA GAC TTA ACA TTG ACT GTA TTA	720
	Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu	
225	230	235
230	235	240
5	GAT ATC GCC GCT TTC TTT CCA AAC TAT GAC AAT AGG AGA TAT CCA ATT	768
	Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile	
	245	250
	250	255
10	CAG CCA GTT GGT CAA CTA ACA AGG GAA GTT TAT ACG GAC CCA TTA ATT	816
	Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile	
	260	265
	265	270
15	AAT TTT AAT CCA CAG TTA CAG TCT GTA GCT CAA TTA CCT ACT TTT AAC	864
	Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn	
	275	280
	280	285
20	GTT ATG GAG AGC AGC GCA ATT AGA AAT CCT CAT TTA TTT GAT ATA TTG	912
	Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu	
	290	295
	295	300
25	AAT AAT CTT ACA ATC TTT ACG GAT TGG TTT AGT GTT GGA CGC AAT TTT	960
	Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe	
	305	310
	310	315
	315	320
30	TAT TGG GGA GGA CAT CGA GTA ATA TCT AGC CTT ATA GGA GGT GGT AAC	1008
	Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Asn	
	325	330
	330	335
35	ATA ACA TCT CCT ATA TAT GGA AGA GAG GCG AAC CAG GAG CCT CCA AGA	1056
	Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg	
	340	345
	345	350
40	TCC TTT ACT TTT AAT GGA CCG GTA TTT AGG ACT TTA TCA AAT CCT ACT	1104
	Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr	
	355	360
	360	365
45	TTA CGA TTA TTA CAG CAA CCT TGG CCA GCG CCA CCA TTT AAT TTA CGT	1152
	Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg	
	370	375
	375	380
50	GGT GTT GAA GGA GTA GAA TTT TCT ACA CCT ACA AAT AGC TTT ACG TAT	1200
	Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr	
	385	390
	390	395
	395	400
55	405	410
	410	415
60	415	
65	AAT AGT GTG CCA CCT CGC GAA TAT AGT CAT CGT TTA TGT CAT GCA	1248
	Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala	
	420	425
	425	430
70	430	

	ACT TTT GTT CAA AGA TCT GGA ACA CCT TTT TTA ACA ACT GGT GTA GTA		1344
	Thr Phe Val Gin Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val		
	435	440	445
5	TTT TCT TGG ACG CAT CGT AGT GCA ACT CTT ACA AAT ACA ATT GAT CCA		1392
	Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro		
	450	455	460
10	GAG AGA ATT AAT CAA ATA CCT TTA GTG AAA GGA TTT AGA GTT TGG GGG		1440
	Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly		
	465	470	475
	Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu		
15	485	490	495
	CGA AGA AAT ACC TTT GGT GAT TTT GTA TCT CTA CAA GTC AAT ATT AAT		1536
	Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn		
	500	505	510
20	TCA CCA ATT ACC CAA AGA TAC CGT TTA AGA TTT CGT TAC GCT TCC AGT		1584
	Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser		
	515	520	525
25	AGG GAT GCA CGA GTT ATA GTA TTA ACA GGA GCG GCA TCC ACA GGA GTG		1632
	Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val		
	530	535	540
30	GGA GGC CAA GTT AGT GTA AAT ATG CCT CTT CAG AAA ACT ATG GAA ATA		1680
	Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile		
	545	550	555
35	560		
	GGG GAG AAC TTA ACA TCT AGA ACA TTT AGA TAT ACC GAT TTT AGT AAT		1728
	Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn		
	565	570	575
	CCT TTT TCA TTT AGA GCT AAT CCA GAT ATA ATT GGG ATA AGT GAA CAA		
	Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln		
	580	585	590
40	CCT CTA TTT GGT GCA GGT TCT ATT AGT AGC GGT GAA CTT TAT ATA GAT		1824
	Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp		
	595	600	605
45	AAA ATT GAA ATT ATT CTA GCA GAT GCA ACA TTT GAA GCA GAA TCT GAT		1872
	Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp		
	610	615	620
50	TTA GAA AGA GCA CAA AAG GCG GTG AAT GCC CTG TTT ACT TCT TCC AAT		1920
	Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn		
	625	630	635
	640		

	CAA ATC GGG TTA AAA ACC GAT GTG ACG GAT TAT CAT ATT GAT CAA GTA Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val 645	650	655	1968
5	TCC AAT TTA GTG GAT TGT TTA TCA GAT GAA TTT TGT CTG GAT GAA AAG Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys 660	665	670	2016
10	CGA GAA TTG TCC GAG AAA GTC AAA CAT GCG AAG CGA CTC AGT GAT GAG Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu 675	680	685	2064
15	CGG AAT TTA CTT CAA GAT CCA AAC TTC AGA GGG ATC AAT AGA CAA CCA Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro 690	695	700	2112
20	GAC CGT GGC TGG AGA GGA AGT ACA GAT ATT ACC ATC CAA GGA GGA GAT Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp 705	710	715	2160
25	GAC GTA TTC AAA GAG AAT TAC GTC ACA CTA CCG GGT ACC GTT GAT GAG Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu 725	730	735	2208
30	TGC TAT CCA ACG TAT TTA TAT CAG AAA ATA GAT GAG TCG AAA TTA AAA Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys 740	745	750	2256
35	GCT TAT ACC CGT TAT GAA TTA AGA GGG TAT ATC GAA GAT AGT CAA GAC Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp 755	760	765	2304
40	TTA GAA ATC TAT TTG ATC CGT TAC AAT GCA AAA CAC GAA ATA GTA AAT Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn 770	775	780	2352
45	GTG CCA GGC ACG GGT TCC TTA TGG CCG CTT TCA GCC CAA AGT CCA ATC Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile 785	790	795	2400
50	GGA AAG TGT GGA GAA CCG AAT CGA TGC GCG CCA CAC CTT GAA TGG AAT Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn 805	810	815	2448
	CCT GAT CTA GAT TGT TCC TGC AGA GAC GGG GAA AAA TGT GCA CAT CAT Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His 820	825	830	2496
	TCC CAT CAT TTC ACC TTG GAT ATT GAT GTT GGA TGT ACA GAC TTA AAT Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn 835	840	845	2544

	GAG GAC TTA GGT GTA TGG GTG ATA TTC AAG ATT AAG ACG CAA GAT GGC Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly 850	855	860	2592
5	CAT GCA AGA CTA GGG AAT CTA GAG TTT CTC GAA GAG AAA CCA TTA TTA His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu 865	870	875	880
10	GGG GAA GCA CTA GCT CGT GTG AAA AGA GCG GAG AAG AAG TGG AGA GAC Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp 885	890	895	2688
15	AAA CGA GAG AAA CTG CAG TTG GAA ACA AAT ATT GTT TAT AAA GAG GCA Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala 900	905	910	2736
20	AAA GAA TCT GTA GAT GCT TTA TTT GTA AAC TCT CAA TAT GAT AGA TTA Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu 915	920	925	2784
25	CAA GTG GAT ACG AAC ATC GCA ATG ATT CAT GCG GCA GAT AAA CGC GTT Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val 930	935	940	2832
30	CAT AGA ATC CGG GAA GCG TAT CTG CCA GAG TTG TCT GTG ATT CCA GGT His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly 945	950	955	2880
35	GTC AAT GCG GCC ATT TTC GAA GAA TTA GAG GGA CGT ATT TTT ACA GCG Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala 965	970	975	2928
40	TAT TCC TTA TAT GAT GCG AGA AAT GTC ATT AAA AAT GGC GAT TTC AAT Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn 980	985	990	2976
45	AAT GGC TTA TTA TGC TGG AAC GTG AAA GGT CAT GTA GAT GTA GAA GAG Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu 995	1000	1005	3024
50	CAA AAC AAC CAC CGT TCG GTC CTT GTT ATC CCA GAA TGG GAG GCA GAA Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu 1010	1015	1020	3072
55	GTG TCA CAA GAG GTT CGT GTC TGT CCA GGT CGT GGC TAT ATC CTT CGT Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg 1025	1030	1035	3120
60	GTC ACA GCA TAT AAA GAG GGA TAT GGA GAG GGC TGC GTA ACG ATC CAT Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His 1045	1050	1055	3168

	GAG ATC GAA GAC AAT ACA GAC GAA CTG AAA TTC AGC AAC TGT GTA GAA Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu 1060	1065	1070	3216
5	GAG GAA GTA TAT CCA AAC AAC ACA GTA ACG TGT AAT AAT TAT ACT GGG Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly 1075	1080	1085	3264
10	ACT CAA GAA GAA TAT GAG GGT ACG TAC ACT TCT CGT AAT CAA GGA TAT Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr 1090	1095	1100	3312
15	GAC GAA GCC TAT GGT AAT AAC CCT TCC GTA CCA GCT GAT TAC GCT TCA Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser 1105	1110	1115	3360
20	GTC TAT GAA GAA AAA TCG TAT ACA GAT GGA CGA AGA GAG AAT CCT TGT Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys 1125	1130	1135	3408
25	GAA TCT AAC AGA GGC TAT GGG GAT TAC ACA CCA CTA CCG GCT GGT TAT Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr 1140	1145	1150	3456
30	GTA ACA AAG GAT TTA GAG TAC TTC CCA GAG ACC GAT AAG GTA TGG ATT Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile 1155	1160	1165	3504
35	GAG ATC GGA GAA ACA GAA GGA ACA TTC ATC GTG GAT AGC GTG GAA TTA Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu 1170	1175	1180	3552
40	CTC CTT ATG GAG GAA Leu Leu Met Glu Glu 1185			3567

(2) INFORMATION FOR SEQ ID NO:61:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1189 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

50 Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
5 10 15

Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn
 20 25 30

	Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn			
	35	40	45	
5	Phe Val Pro Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp			
	50	55	60	
	Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu			
	65	70	75	80
10	Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile			
	85	90	95	
	Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala			
	100	105	110	
15	Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg			
	115	120	125	
20	Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile			
	130	135	140	
25	Pro Ser Phe Asp Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr			
	145	150	155	160
30	Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile			
	165	170	175	
35	Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr			
	180	185	190	
40	Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn			
	195	200	205	
45	Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Ala Ser Thr Tyr Gln Asp			
	210	215	220	
50	Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu			
	225	230	235	240
55	Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile			
	245	250	255	
60	Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile			
	260	265	270	
65	Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn			
	275	280	285	
70	Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu			
	290	295	300	
75	Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe			
	305	310	315	320

	Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Gly Asn			
	325	330	335	
	Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg			
5	340	345	350	
	Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr			
	355	360	365	
10	Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg			
	370	375	380	
	Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr			
	385	390	395	400
15	Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp			
	405	410	415	
20	Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala			
	420	425	430	
25	Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val			
	435	440	445	
30	Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro			
	450	455	460	
35	Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly			
	465	470	475	480
40	Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu			
	485	490	495	
45	Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn			
	500	505	510	
50	Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser			
	515	520	525	
55	Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val			
	530	535	540	
60	Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile			
	545	550	555	560
65	Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn			
	565	570	575	
70	Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln			
	580	585	590	
75	Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp			
	595	600	605	

Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp
 610 615 620

5 Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn
 625 630 635 640

Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val
 645 650 655

10 Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys
 660 665 670

Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu
 675 680 685

15 Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro
 690 695 700

20 Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp
 705 710 715 720

Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu
 725 730 735

25 Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys
 740 745 750

Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp
 755 760 765

30 Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn
 770 775 780

35 Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile
 785 790 795 800

Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn
 805 810 815

40 Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His
 820 825 830

Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn
 835 840 845

45 Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly
 850 855 860

His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu
 865 870 875 880

Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp
 885 890 895

Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala
 900 905 910

5 Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu
 915 920 925

Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val
 930 935 940

10 His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly
 945 950 955 960

Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala
 965 970 975

15 Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn
 980 985 990

20 Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu
 995 1000 1005

25 Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu
 1010 1015 1020

30 Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg
 1025 1030 1035 1040

35 Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His
 1045 1050 1055

Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu
 1060 1065 1070

40 Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly
 1075 1080 1085

Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr
 1090 1095 1100

Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser
 1105 1110 1115 1120

Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys
 1125 1130 1135

45 Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
 1140 1145 1150

50 Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile
 1155 1160 1165

Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
 1170 1175 1180

Leu Leu Met Glu Glu
1185

5 (2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

15 CGGGGATTAA ATAATTTACC GGCTAGCACG TATCAAGATT GGATAAC

47

(2) INFORMATION FOR SEQ ID NO:63:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
26 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CGGGGATTAA ATAATTTACC GAAAAACGTA TCAAGATTGG ATAAC

45

30 (2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

40 GGATAGCACT CATCAAAGGT ACC

23

45 (2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
50 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CGGGGATTAA ATAATACCGA AAAGCACGTA TCAAGATTGG ATAAC

45

20 (2) INFORMATION FOR SEQ ID NO:66:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CGGGGATTAA ATAATTAAA AAAGCACGTA TCAAGATTGG ATAAC

45

15 (2) INFORMATION FOR SEQ ID NO:67:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CGGGGATTAA ATAATTACC GAAGCACGTA TCAAGATTGG ATAAC

45

30 (2) INFORMATION FOR SEQ ID NO:68:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GGATTAATA ATTTACCGAA AAGCATATCA AGATTGGATA ACATATAATC G

51

45 (2) INFORMATION FOR SEQ ID NO:69:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GGATTAATA ATTTACCGAA AAGCACGACA AGATTGGATA ACATATAATC G

51

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GATTCTGTAA TTTTAGAAA GATGGGGATT GACAACGATA AATGTCAATG

50

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GATTCTGTAA TTTTGGAAA GATGGGGATT GACAACGATA AATGTCAATG

50

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GATTCTGTAA TTTTGGAGA AATGGGGATT GACAACGATA AATGTCAATG

50

40 (2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

50 TCTGTAATT TTGGAGAAAG AAGGATTGAC AACGATAAAAT GTCAATGAAA AC

52

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GTAATTTTG GAGAAAGATG GATTGACAAC GATAAAATGTC AATGAAAAC

49

10

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GTAATTTTG GAGAAAGATG GGGAAACAAAC GATAAATGTC AATGAAAAC 49

25 (2) INFORMATION FOR SEQ ID NO: 76:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GTAATTTTG GAGAAAGATG GGGATTGAAC GATAAAATGTC AATGAAAAC 49

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